



# STIC Search Report

Biotech-Chem Library

## STIC Database Tracking

TO: Anne Holleran  
Location: o 8E03; m 8E12  
Art Unit: 1642  
Tuesday, July 08, 2003  
Case Serial Number: 09/822295

From: Barb O'Bryen  
Location: Biotech-Chem Library  
CM1-6A05  
Phone: 308-4291  
barbara.obryen@uspto.gov

## Search Notes





PI Markby D., Ernst S., Peles E., Plozman G;  
 DR WPI: 1999-009444/01.  
 XX  
 XX New nucleic acid encoding specific protein tyrosine phosphatases  
 PT useful for identifying specific modulators for treatment and  
 PT prevention of cancer and neurodegenerative disease  
 PI  
 XX  
 XX Example 4: Page 81; 199pp; English.  
 CC The present invention describes isolated, enriched or purified nucleic  
 CC acids encoding ptp04, SAB, ptp05, ptp10, A-P and ALK-7 proteins. The  
 CC above proteins, other than ALK-7, are protein tyrosine phosphatases  
 CC (PTPs) and are used to identify substances that modulate their activity  
 CC (i.e. agonists and antagonists), including NRP) in vivo or in vitro.  
 CC These substances are used to treat or prevent diseases associated with  
 CC abnormal signal transduction pathways that involve the proteins,  
 CC particularly cancer (e.g. leukemia and lymphoma), while modulators of  
 CC ALK-7 (which is a type I receptor serine/threonine kinase) are used to  
 CC promote neuronal survival, particularly for treating Alzheimer's,  
 CC Parkinson's or Huntington's diseases. Nucleic acid fragments of the  
 CC polynucleotides encoding the proteins can be used as probes to identify  
 CC and clone related sequences; to detect protein-encoded RNA; to generate  
 CC transgenic animals and in gene therapy (optionally after mutation). Ab  
 CC are used to determine the proteins. The present sequence represents a  
 CC human PTP04 peptide from the present invention.  
 XX  
 SQ Sequence 31 AA:  
 Query Match 100.0%; Score 165; DB 20; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1,90-17;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SWPPSCTSSKMSLDDLPERQDGVTPPSLLP 31  
 DQ 1 SWPPSCTSSKMSLDDLPERQDGVTPPSLLP 31  
 RESULT 2  
 AAY28654  
 ID AAY28654 standard; Protein: 692 AA.  
 AC AAY28654;  
 XX  
 XX 01-OCT-1999 (first entry)  
 DT Human cytoplasmic phosphatase, Lyp2 protein.  
 DE  
 XX  
 KW Lymphoid Protein Tyrosine Phosphatase; Lyp protein; immunosuppressant;  
 KW intracellular tyrosine phosphatase; pipase, fetal liver; transplant;  
 KW resting lymphoid cell; protein tyrosine kinase; ptk; lymphocyte;  
 KW T cell antigen receptor signalling; cytokine receptor signalling;  
 KW autoimmune disease; intronic sequence; alternative mRNA splicing.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Localization/Qualifiers  
 FT Domain 27..289  
 FT /label= ptpase domain  
 FT /note= "Single catalytic protein tyrosine phosphatase  
 FT domain"  
 FT Domain 469..472  
 FT /label= NXY\_motif  
 FT /note= "unique sequence recognised by phosphotyrosine  
 FT binding (PTB) domain"  
 FT Binding-site 615..623  
 FT /label= SH2 binding site  
 FT /note= "protein tyrosine phosphory"  
 XX  
 XX W09946548-A1.  
 PN  
 XX  
 XX 22-JUL-1999.  
 PD  
 XX

DE 18 JAN 1999; 99W 04A00008.  
 XX  
 XX 16 JAN 1999; 98W 22000000.  
 XX  
 XX (HSCR) HSC RES & DEV LP.  
 XX  
 XX Rofman CW;  
 XX  
 XX WPI: 1999 444404/01.  
 DR N PSDB; AAX90500.  
 XX  
 XX New nucleic acid encoding intracellular tyrosine phosphatase and  
 PT related proteins, used to modulate signalling for cancer therapy,  
 PT particularly as immunosuppressant  
 XX  
 XX Claim 4b; Page 55; 105pp; English.  
 PS  
 XX The present protein sequence is that of the cytochrome b5 domain of  
 CC protein tyrosine phosphatase, Lyp2 protein, that has a kinase catalytic  
 CC domain. The non-catalytic portion of the phosphatase contains unique  
 CC sequences, including a single PEST sequence (residues 171-177), a WY  
 CC and Thr. It is expressed specifically in fetal liver and in resting  
 CC lymphoid cells. Lyp2 is an isoform of the Lyp protein that is highly  
 CC alternative splicing of the mRNA. The intronic region of Lyp2 encodes  
 CC for the C-terminal 7 amino acids and part of the conserved region of  
 CC Lyp2. Lyp2 shares sequence identity with the native phosphatase, Lyp1  
 CC Lyp proteins are important for regulation of cell growth and signal  
 CC receptor signalling and for early and late stages of T cell  
 CC differentiation. Lyp2 has immunosuppressive activity and is able that  
 CC increase expression of Lyp protein can be used as means of preventing  
 CC agents to reduce or prevent T cell activation or proliferation in  
 CC control thymocyte differentiation, to treat and modulate leukemia and  
 CC transplant situations.  
 XX  
 SQ Sequence 692 AA:  
 Query Match 90.0%; Score 146.5; DB 20; Length 692;  
 Best Local Similarity 90.0%; Pred. No. 190-190;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SWPPSCTSSKMSLDDLPERQDGVTPPSLLP 41  
 DQ 640 SWPPSCTSSKMSLDDLPERQDGVTPPSLLP 640  
 RESULT 3  
 AAY378624  
 ID AAY378624 standard; Protein: 799 AA.  
 AC AAY378624;  
 XX  
 XX 04-JAN-2001 (first entry)  
 DT Human tyrosine phosphatase.  
 DE  
 XX  
 XX Human tyrosine phosphatase; LYP.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX ONI 632899 A.  
 DR  
 XX  
 XX 11-JUL-2001.  
 PD  
 XX 29-OCT-1999; 99W 01100000.  
 XX  
 XX 29-OCT-1999; 99W 01100000.  
 XX  
 XX (W09946548-A1) HUMAN CYTOCHROME b5  
 XX  
 XX Ren S., Wu L., Qian B.  
 PT  
 XX WPI: 2001 000000/01.  
 DR  
 XX N PSDB; AAX90500.











```

PR 20-JUL-1999; 990S-0144642;
PR 20-JUL-1999; 990S-0144644;
PR 20-JUL-1999; 990S-0144814;
PR 20-JUL-1999; 990S-0145096;
PR 20-JUL-1999; 990S-0145088;
PR 20-JUL-1999; 990S-0145085;
PR 20-JUL-1999; 990S-0145087;
PR 20-JUL-1999; 990S-0145089;
PR 20-JUL-1999; 990S-0145192;
PR 20-JUL-1999; 990S-0145187;
PR 20-JUL-1999; 990S-0145284;
PR 20-JUL-1999; 990S-0145276;
PR 20-JUL-1999; 990S-0145913;
PR 20-JUL-1999; 990S-0145918;
PR 27-JUL-1999; 990S-0145911;
PR 27-JUL-1999; 990S-0145917;
PR 02-AUG-1999; 990S-0145885;
PR 02-AUG-1999; 990S-0145884;
PR 03-AUG-1999; 990S-0147008;
PR 04-AUG-1999; 990S-0147204;
PR 04-AUG-1999; 990S-0147302;
PR 05-AUG-1999; 990S-0147192;
PR 05-AUG-1999; 990S-0147260;
PR 05-AUG-1999; 990S-0147303;
PR 05-AUG-1999; 990S-0147416;
PR 05-AUG-1999; 990S-0147454;
PR 05-AUG-1999; 990S-0147456;
PR 05-AUG-1999; 990S-0147458;
PR 05-AUG-1999; 990S-0148311;
PR 05-AUG-1999; 990S-0148341;
PR 05-AUG-1999; 990S-0148565;
PR 05-AUG-1999; 990S-0148684;
PR 05-AUG-1999; 990S-0149368;
PR 05-AUG-1999; 990S-0149419;
PR 05-AUG-1999; 990S-0149426;
PR 05-AUG-1999; 990S-0149722;
PR 05-AUG-1999; 990S-0149725;
PR 05-AUG-1999; 990S-0149902;
PR 05-AUG-1999; 990S-0149902;
PR 05-AUG-1999; 990S-0151083;
PR 05-AUG-1999; 990S-0151083;
PR 05-AUG-1999; 990S-0151303;
PR 05-AUG-1999; 990S-0151439;
PR 05-AUG-1999; 990S-0151543;
PR 05-AUG-1999; 990S-0152363;
PR 05-AUG-1999; 990S-0153027;
PR 05-AUG-1999; 990S-0153758;
PR 05-AUG-1999; 990S-0154013;
PR 05-AUG-1999; 990S-0154339;
PR 05-AUG-1999; 990S-0154779;
PR 05-AUG-1999; 990S-0155139;
PR 05-AUG-1999; 990S-0155486;
PR 05-AUG-1999; 990S-0155459;
PR 05-AUG-1999; 990S-0155458;
PR 05-AUG-1999; 990S-0155456;
PR 05-AUG-1999; 990S-0155711;
PR 05-AUG-1999; 990S-0157751;
PR 05-AUG-1999; 990S-0157865;
PR 05-AUG-1999; 990S-0158029;
PR 05-AUG-1999; 990S-0158237;
PR 05-AUG-1999; 990S-0158466;
PR 05-AUG-1999; 990S-0159329;
PR 05-AUG-1999; 990S-0159296;
PR 05-AUG-1999; 990S-0159426;
PR 05-AUG-1999; 990S-0159430;
PR 05-AUG-1999; 990S-0159431;

```

---

```

PR 14-OCT-1999; 990S-0159637;
PR 14-OCT-1999; 990S-0159638;
PR 18-OCT-1999; 990S-0159754;
PR 21-OCT-1999; 990S-0160741;
PR 21-OCT-1999; 990S-0160747;
PR 21-OCT-1999; 990S-0160768;
PR 21-OCT-1999; 990S-0160770;
PR 21-OCT-1999; 990S-0160814;
PR 21-OCT-1999; 990S-0160815;
PR 22-OCT-1999; 990S-0160980;
PR 22-OCT-1999; 990S-0160981;
PR 22-OCT-1999; 990S-0160989;
PR 25-OCT-1999; 990S-0161404;
PR 25-OCT-1999; 990S-0161405;
PR 25-OCT-1999; 990S-0161406;
PR 26-OCT-1999; 990S-0161359;
PR 26-OCT-1999; 990S-0161360;
PR 26-OCT-1999; 990S-0161361;
PR 28-OCT-1999; 990S-0161920;
PR 28-OCT-1999; 990S-0161992;
PR 28-OCT-1999; 990S-0161993;
PR 29-OCT-1999; 990S-0162142;

```

Query Match 33.98; Score 50; DB 21; Length 513;  
Post Local Similarity 42.98; Fred. 80; 9.6;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

```

QY 1 SMPSCGSSKMSIDPPEKQ 21
DE 6 SWTPGVAVKAMPVLPPEKE 26

```

RESUME 11  
AA52712 standard; Protein, 521 AA.  
XX  
AC AA52712;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67938.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
FW hybridization assay; specific mutation; gene expression control; promoter;  
XX  
XX Arabidopsis thaliana.  
OS  
FN EP1033405-A2.  
XX  
XX  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP 0301439.  
XX  
PR 25-FEB-1999; 990S-0121825;  
PR 05-MAR-1999; 990S-0123180;  
PR 09-MAR-1999; 990S-0123548;  
PR 23-MAR-1999; 990S-0125788;  
PR 25-MAR-1999; 990S-0126264;  
PR 29-MAR-1999; 990S-0126785;  
PR 01-APR-1999; 990S-0127462;  
PR 06-APR-1999; 990S-0128234;  
PR 08-APR-1999; 990S-0128714;  
PR 10-APR-1999; 990S-0129845;  
PR 19-APR-1999; 990S-0130077;  
PR 21-APR-1999; 990S-0130449;  
PR 23-APR-1999; 990S-0130510;  
PR 28-APR-1999; 990S-0130849;  
PR 30-APR-1999; 990S-0131441;  
PR 30-APR-1999; 990S-0132048;  
PR 30-APR-1999; 990S-0132407;  
PR 04-MAY-1999; 990S-0132484;  
PR 05-MAY-1999; 990S-0132485;

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----







15 With: 1000 12.000/10.

XX New isolated human genes and the secreted polypeptides they encode -  
 16 isolated for diagnosis and treatment of e.g. cancers, neurological  
 17 disorders, immune diseases, inflammation or blood disorders  
 XX  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100

biochemicals: Para 105: 46497: English.  
 This sequence represents a fragment of a secreted human protein encoded  
 by the nucleotide molecule detailed in the descriptor line. The gene  
 can be used to generate fusion proteins by linking to the gene to a  
 human immunoglobulin Fc portion (e.g. AAX27302) for increasing the  
 stability of the fused protein as compared to the human protein only.  
 The invention relates to 123 novel genes and their fragments (nucleic  
 acid sequences: AAX27311-A27344; amino acid sequences: AAV02650-Y02788)  
 which are useful for preventing, treating or ameliorating medical  
 conditions caused by protein or gene therapy. Also, pathological  
 conditions can be diagnosed by determining the amount of the new  
 polypeptides in a sample or by determining the presence of mutations in  
 the new polypeptides. Specific uses are described for each of the 123  
 polypeptides, based on which tissues they are most highly expressed in  
 (see AAX27411 for described uses).

XX  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200

Seq: 1000 12.000/10. Score 52.5; DB 20; Length 57;  
 Best Local Similarity 60.0%; Prod. No. 2.5;  
 Mismatches 12; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

XX  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200

Search completed: July 8, 2003, 12:09:46  
 Job time: 62.417 secs



## M protein - protein search, using sw model

Genome version 5.1.6  
 Available (c) 1993 - 2003 Compen Ltd.

Run on: July 8, 2004, 12:08:17 : Search time 14.985 Seconds  
 (without alignments)  
 60.852 Million cell updates/sec

Initial  
 Percent score: 105  
 Sequence: 1 SWPSTSSKSMILHLEKQKIVPSSILP 31

Score: 1.000 : Gapopen 0.5  
 Gapopen 10.0 : Gapext 0.5

Short Read: 27,574 seqs, 294,229,22 residues

Total number of hits satisfying chosen parameters: 262574

Minimum E score: 0  
 Maximum E score: 2500000000

Post Processing: Minimum Match: 0.8  
 Maximum Match: 1.00  
 Listing first 45 summaries

Database: 1: us-09-822-295-15  
 2: us-09-822-295-15  
 3: us-09-822-295-15  
 4: us-09-822-295-15  
 5: us-09-822-295-15  
 6: us-09-822-295-15  
 7: us-09-822-295-15  
 8: us-09-822-295-15  
 9: us-09-822-295-15  
 10: us-09-822-295-15  
 11: us-09-822-295-15  
 12: us-09-822-295-15  
 13: us-09-822-295-15  
 14: us-09-822-295-15  
 15: us-09-822-295-15  
 16: us-09-822-295-15  
 17: us-09-822-295-15  
 18: us-09-822-295-15  
 19: us-09-822-295-15  
 20: us-09-822-295-15  
 21: us-09-822-295-15  
 22: us-09-822-295-15  
 23: us-09-822-295-15  
 24: us-09-822-295-15  
 25: us-09-822-295-15  
 26: us-09-822-295-15  
 27: us-09-822-295-15  
 28: us-09-822-295-15  
 29: us-09-822-295-15  
 30: us-09-822-295-15  
 31: us-09-822-295-15  
 32: us-09-822-295-15  
 33: us-09-822-295-15  
 34: us-09-822-295-15  
 35: us-09-822-295-15  
 36: us-09-822-295-15  
 37: us-09-822-295-15  
 38: us-09-822-295-15  
 39: us-09-822-295-15  
 40: us-09-822-295-15  
 41: us-09-822-295-15  
 42: us-09-822-295-15  
 43: us-09-822-295-15  
 44: us-09-822-295-15  
 45: us-09-822-295-15

## SUMMARIES

Result No.	Score	Query	Match	Length	DE	ID	Description
1	100.0	100.0	41	4	US-09-081-345-15	Sequence 15, App	
2	100.0	100.0	807	4	US-09-081-345-2	Sequence 2, Appl	
3	88.5	88.5	802	4	US-09-081-345-18	Sequence 18, App	
4	64.4	64.4	474	4	US-09-069-023-31	Sequence 31, App	
5	62.6	62.6	57	4	US-09-227-357-534	Sequence 534, App	
6	60.5	60.5	789	4	US-08-971-188-9	Sequence 9, Appl	
7	60.5	60.5	789	4	US-08-971-188-9	Sequence 9, App	
8	60.4	60.4	896	4	US-08-501-126-2	Sequence 22, App	
9	49.5	49.5	4551	4	US-09-320-878-1	Sequence 1, Appl	
10	49.5	49.5	4613	4	US-09-105-537-31	Sequence 31, App	
11	49.5	49.5	11877	4	US-09-105-537-6	Sequence 6, Appl	
12	48.5	48.5	337	4	US-09-042-337-2	Sequence 2, Appl	
13	48	48	373	4	US-09-268-992-45	Sequence 45, App	
14	48	48	373	4	US-09-268-992-45	Sequence 45, App	
15	48	48	374	4	US-09-268-992-43	Sequence 43, App	
16	48	48	374	4	US-09-268-992-43	Sequence 43, App	
17	48	48	450	4	US-09-268-992-41	Sequence 41, App	
18	48	48	450	4	US-09-268-992-41	Sequence 41, App	
19	48	48	450	4	US-09-268-992-39	Sequence 39, App	
20	48	48	450	4	US-09-268-992-39	Sequence 39, App	
21	48	48	476	4	US-09-188-579-114	Sequence 114, App	
22	48	48	476	4	US-09-188-579-114	Sequence 114, App	
23	48	48	476	4	US-09-315-444-114	Sequence 114, App	
24	48	48	476	4	US-09-315-444-114	Sequence 114, App	
25	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
26	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
27	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
28	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
29	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
30	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
31	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
32	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
33	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
34	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
35	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
36	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
37	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
38	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
39	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
40	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
41	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
42	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
43	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
44	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	
45	48	48	476	4	US-08-677-298-2	Sequence 2, Appl	

## ALIGNMENTS

RESULT 1  
 US-09-081-345-15  
 Sequence 15, Application US-09081345  
 Patent No. 6228641  
 GENERAL INFORMATION:  
 APPLICANT: Bahlia Tallal  
 APPLICANT: Gregory D. Ploman  
 TITLE OF INVENTION: Treatment and prevention of  
 NUMBER OF SEQUENCES: 18  
 CURRENCE/SEQUENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2056  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 MEDIUM TYPE: Storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASTSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 09/09081345  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/047,222  
 FILING DATE: May 20, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wardburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REGISTRATION NUMBER: 2,4253  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELNET: 67-3510  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-081-345-15  
 Query Match: 100.0% Score 165.4 PH 4.7 Length 41  
 Post Local Similarity: 100.0% Prod. No. 3,50-195

1 NAME: [REDACTED] ADDRESS: [REDACTED]  
 2 ADDRESS: [REDACTED]  
 3 STREET: [REDACTED]  
 4 CITY: [REDACTED]  
 5 STATE: [REDACTED]  
 6 COUNTRY: [REDACTED]  
 7 ZIP: [REDACTED]  
 8 COMPUTER READABLE FORM:  
 9 RECORD TYPE: [REDACTED]  
 10 MEDIUM TYPE: [REDACTED]  
 11 OPERATING SYSTEM: [REDACTED]  
 12 SOFTWARE: [REDACTED]  
 13 CURRENT APPLICATION DATA:  
 14 FILING DATE: [REDACTED]  
 15 CLASSIFICATION:  
 16 PRIORITY APPLICATION DATA:  
 17 APPLICATION NUMBER: [REDACTED]  
 18 FILING DATE: [REDACTED]  
 19 ATTORNEY/AGENT INFORMATION:  
 20 NAME: [REDACTED]  
 21 REGISTRATION NUMBER: [REDACTED]  
 22 RETIREMENT/STATUS: [REDACTED]  
 23 TELEPHONE: [REDACTED]  
 24 TELEFAX: [REDACTED]  
 25 FAX: [REDACTED]  
 26 INFORMATION FOR SEQ ID NO: 1:  
 27 SEQUENCE CHARACTERISTICS:  
 28 LENGTH: 802 amino acids  
 29 TYPE: amino acid  
 30 STRANDEDNESS: single  
 31 TOPOLOGY: linear  
 32 MOLECULE TYPE: peptide  
 33 US-09-081-345-1B  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525  
 526  
 527  
 528  
 529  
 530  
 531  
 532  
 533  
 534  
 535  
 536  
 537  
 538  
 539  
 540  
 541  
 542  
 543  
 544  
 545  
 546  
 547  
 548  
 549  
 550  
 551  
 552  
 553  
 554  
 555  
 556  
 557  
 558  
 559  
 560  
 561  
 562  
 563  
 564  
 565  
 566  
 567  
 568  
 569  
 570  
 571  
 572  
 573  
 574  
 575  
 576  
 577  
 578  
 579  
 580  
 581  
 582  
 583  
 584  
 585  
 586  
 587  
 588  
 589  
 590  
 591  
 592  
 593  
 594  
 595  
 596  
 597  
 598  
 599  
 600  
 601  
 602  
 603  
 604  
 605  
 606  
 607  
 608  
 609  
 610  
 611  
 612  
 613  
 614  
 615  
 616  
 617  
 618  
 619  
 620  
 621  
 622  
 623  
 624  
 625  
 626  
 627  
 628  
 629  
 630  
 631  
 632  
 633  
 634  
 635  
 636  
 637  
 638  
 639  
 640  
 641  
 642  
 643  
 644  
 645  
 646  
 647  
 648  
 649  
 650  
 651  
 652  
 653  
 654  
 655  
 656  
 657  
 658  
 659  
 660  
 661  
 662  
 663  
 664  
 665  
 666  
 667  
 668  
 669  
 670  
 671  
 672  
 673  
 674  
 675  
 676  
 677  
 678  
 679  
 680  
 681  
 682  
 683  
 684  
 685  
 686  
 687  
 688  
 689  
 690  
 691  
 692  
 693  
 694  
 695  
 696  
 697  
 698  
 699  
 700  
 701  
 702  
 703  
 704  
 705  
 706  
 707  
 708  
 709  
 710  
 711  
 712  
 713  
 714  
 715  
 716  
 717  
 718  
 719  
 720  
 721  
 722  
 723  
 724  
 725  
 726  
 727  
 728  
 729  
 730  
 731  
 732  
 733  
 734  
 735  
 736  
 737  
 738  
 739  
 740  
 741  
 742  
 743  
 744  
 745  
 746  
 747  
 748  
 749  
 750  
 751  
 752  
 753  
 754  
 755  
 756  
 757  
 758  
 759  
 760  
 761  
 762  
 763  
 764  
 765  
 766  
 767  
 768  
 769  
 770  
 771  
 772  
 773  
 774  
 775  
 776  
 777  
 778  
 779  
 780  
 781  
 782  
 783  
 784  
 785  
 786  
 787  
 788  
 789  
 790  
 791  
 792  
 793  
 794  
 795  
 796  
 797  
 798  
 799  
 800  
 801  
 802  
 803  
 804  
 805  
 806  
 807  
 808  
 809  
 810  
 811  
 812  
 813  
 814  
 815  
 816  
 817  
 818  
 819  
 820  
 821  
 822  
 823  
 824  
 825  
 826  
 827  
 828  
 829  
 830  
 831  
 832  
 833  
 834  
 835  
 836  
 837  
 838  
 839  
 840  
 841  
 842  
 843  
 844  
 845  
 846  
 847  
 848  
 849  
 850  
 851  
 852  
 853  
 854  
 855  
 856  
 857  
 858  
 859  
 860  
 861  
 862  
 863  
 864  
 865  
 866  
 867  
 868  
 869  
 870  
 871  
 872  
 873  
 874  
 875  
 876  
 877  
 878  
 879  
 880  
 881  
 882  
 883  
 884  
 885  
 886  
 887  
 888  
 889  
 890  
 891  
 892  
 893  
 894  
 895  
 896  
 897  
 898  
 899  
 900  
 901  
 902  
 903  
 904  
 905  
 906  
 907  
 908  
 909  
 910  
 911  
 912  
 913  
 914  
 915  
 916  
 917  
 918  
 919  
 920  
 921  
 922  
 923  
 924  
 925  
 926  
 927  
 928  
 929  
 930  
 931  
 932  
 933  
 934  
 935  
 936  
 937  
 938  
 939  
 940  
 941  
 942  
 943  
 944  
 945  
 946  
 947  
 948  
 949  
 950  
 951  
 952  
 953  
 954  
 955  
 956  
 957  
 958  
 959  
 960  
 961  
 962  
 963  
 964  
 965  
 966  
 967  
 968  
 969  
 970  
 971  
 972  
 973  
 974  
 975  
 976  
 977  
 978  
 979  
 980  
 981  
 982  
 983  
 984  
 985  
 986  
 987  
 988  
 989  
 990  
 991  
 992  
 993  
 994  
 995  
 996  
 997  
 998  
 999  
 1000

1 NUMBER OF SEQUENCES: 18  
 2 CYRILIC/ROMAN/ADDRESS:  
 3 ADDRESS: 1501 S Lyon  
 4 STREET: 543 West 44th Street  
 5 STREET: Suite 4700  
 6 CITY: Los Angeles  
 7 STATE: California  
 8 COUNTRY: U.S.A.  
 9 ZIP: 90071-2066  
 10 COMPUTER READABLE FORM:  
 11 RECORD TYPE: 1.25 1.5 1.75 1.9 2.1 2.3 2.5 2.7 2.9 3.1 3.3 3.5 3.7 3.9 4.1 4.3 4.5 4.7 4.9 5.1 5.3 5.5 5.7 5.9 6.1 6.3 6.5 6.7 6.9 7.1 7.3 7.5 7.7 7.9 8.1 8.3 8.5 8.7 8.9 9.1 9.3 9.5 9.7 9.9 10.1 10.3 10.5 10.7 10.9 11.1 11.3 11.5 11.7 11.9 12.1 12.3 12.5 12.7 12.9 13.1 13.3 13.5 13.7 13.9 14.1 14.3 14.5 14.7 14.9 15.1 15.3 15.5 15.7 15.9 16.1 16.3 16.5 16.7 16.9 17.1 17.3 17.5 17.7 17.9 18.1 18.3 18.5 18.7 18.9 19.1 19.3 19.5 19.7 19.9 20.1 20.3 20.5 20.7 20.9 21.1 21.3 21.5 21.7 21.9 22.1 22.3 22.5 22.7 22.9 23.1 23.3 23.5 23.7 23.9 24.1 24.3 24.5 24.7 24.9 25.1 25.3 25.5 25.7 25.9 26.1 26.3 26.5 26.7 26.9 27.1 27.3 27.5 27.7 27.9 28.1 28.3 28.5 28.7 28.9 29.1 29.3 29.5 29.7 29.9 30.1 30.3 30.5 30.7 30.9 31.1 31.3 31.5 31.7 31.9 32.1 32.3 32.5 32.7 32.9 33.1 33.3 33.5 33.7 33.9 34.1 34.3 34.5 34.7 34.9 35.1 35.3 35.5 35.7 35.9 36.1 36.3 36.5 36.7 36.9 37.1 37.3 37.5 37.7 37.9 38.1 38.3 38.5 38.7 38.9 39.1 39.3 39.5 39.7 39.9 40.1 40.3 40.5 40.7 40.9 41.1 41.3 41.5 41.7 41.9 42.1 42.3 42.5 42.7 42.9 43.1 43.3 43.5 43.7 43.9 44.1 44.3 44.5 44.7 44.9 45.1 45.3 45.5 45.7 45.9 46.1 46.3 46.5 46.7 46.9 47.1 47.3 47.5 47.7 47.9 48.1 48.3 48.5 48.7 48.9 49.1 49.3 49.5 49.7 49.9 50.1 50.3 50.5 50.7 50.9 51.1 51.3 51.5 51.7 51.9 52.1 52.3 52.5 52.7 52.9 53.1 53.3 53.5 53.7 53.9 54.1 54.3 54.5 54.7 54.9 55.1 55.3 55.5 55.7 55.9 56.1 56.3 56.5 56.7 56.9 57.1 57.3 57.5 57.7 57.9 58.1 58.3 58.5 58.7 58.9 59.1 59.3 59.5 59.7 59.9 60.1 60.3 60.5 60.7 60.9 61.1 61.3 61.5 61.7 61.9 62.1 62.3 62.5 62.7 62.9 63.1 63.3 63.5 63.7 63.9 64.1 64.3 64.5 64.7 64.9 65.1 65.3 65.5 65.7 65.9 66.1 66.3 66.5 66.7 66.9 67.1 67.3 67.5 67.7 67.9 68.1 68.3 68.5 68.7 68.9 69.1 69.3 69.5 69.7 69.9 70.1 70.3 70.5 70.7 70.9 71.1 71.3 71.5 71.7 71.9 72.1 72.3 72.5 72.7 72.9 73.1 73.3 73.5 73.7 73.9 74.1 74.3 74.5 74.7 74.9 75.1 75.3 75.5 75.7 75.9 76.1 76.3 76.5 76.7 76.9 77.1 77.3 77.5 77.7 77.9 78.1 78.3 78.5 78.7 78.9 79.1 79.3 79.5 79.7 79.9 80.1 80.3 80.5 80.7 80.9 81.1 81.3 81.5 81.7 81.9 82.1 82.3 82.5 82.7 82.9 83.1 83.3 83.5 83.7 83.9 84.1 84.3 84.5 84.7 84.9 85.1 85.3 85.5 85.7 85.9 86.1 86.3 86.5 86.7 86.9 87.1 87.3 87.5 87.7 87.9 88.1 88.3 88.5 88.7 88.9 89.1 89.3 89.5 89.7 89.9 90.1 90.3 90.5 90.7 90.9 91.1 91.3 91.5 91.7 91.9 92.1 92.3 92.5 92.7 92.9 93.1 93.3 93.5 93.7 93.9 94.1 94.3 94.5 94.7 94.9 95.1 95.3 95.5 95.7 95.9 96.1 96.3 96.5 96.7 96.9 97.1 97.3 97.5 97.7 97.9 98.1 98.3 98.5 98.7 98.9 99.1 99.3 99.5 99.7 99.9 100.1 100.3 100.5 100.7 100.9 101.1 101.3 101.5 101.7 101.9 102.1 102.3 102.5 102.7 102.9 103.1 103.3 103.5 103.7 103.9 104.1 104.3 104.5 104.7 104.9 105.1 105.3 105.5 105.7 105.9 106.1 106.3 106.5 106.7 106.9 107.1 107.3 107.5 107.7 107.9 108.1 108.3 108.5 108.7 108.9 109.1 109.3 109.5 109.7 109.9 110.1 110.3 110.5 110.7 110.9 111.1 111.3 111.5 111.7 111.9 112.1 112.3 112.5 112.7 112.9 113.1 113.3 113.5 113.7 113.9 114.1 114.3 114.5 114.7 114.9 115.1 115.3 115.5 115.7 115.9 116.1 116.3 116.5 116.7 116.9 117.1 117.3 117.5 117.7 117.9 118.1 118.3 118.5 118.7 118.9 119.1 119.3 119.5 119.7 119.9 120.1 120.3 120.5 120.7 120.9 121.1 121.3 121.5 121.7 121.9 122.1 122.3 122.5 122.7 122.9 123.1 123.3 123.5 123.7 123.9 124.1 124.3 124.5 124.7 124.9 125.1 125.3 125.5 125.7 125.9 126.1 126.3 126.5 126.7 126.9 127.1 127.3 127.5 127.7 127.9 128.1 128.3 128.5 128.7 128.9 129.1 129.3 129.5 129.7 129.9 130.1 130.3 130.5 130.7 130.9 131.1 131.3 131.5 131.7 131.9 132.1 132.3 132.5 132.7 132.9 133.1 133.3 133.5 133.7 133.9 134.1 134.3 134.5 134.7 134.9 135.1 135.3 135.5 135.7 135.9 136.1 136.3 136.5 136.7 136.9 137.1 137.3 137.5 137.7 137.9 138.1 138.3 138.5 138.7 138.9 139.1 139.3 139.5 139.7 139.9 140.1 140.3 140.5 140.7 140.9 141.1 141.3 141.5 141.7 141.9 142.1 142.3 142.5 142.7 142.9 143.1 143.3 143.5 143.7 143.9 144.1 144.3 144.5 144.7 144.9 145.1 145.3 145.5 145.7 145.9 146.1 146.3 146.5 146.7 146.9 147.1 147.3 147.5 147.7 147.9 148.1 1











Sequence version 5.1.6  
 Copyright (c) 1993 - 2003 CompuGen Ltd.

Method: Protein search, using SW model

Run on: 01/07/03, 12:11:42 : Search time 27 sec4 seconds  
 (without alignments)  
 130,793 Million cell updates/sec

Matrix: US-09-822-295-15  
 165  
 SWPSSTSKMSIDPPPKDQTVPSILTP 31

Scoring table:  
 Gapop: 10.0, Gapext: 0.5

Score: 445758 seqs: 13649773 residues 445758  
 Total number of hits satisfying chosen parameters.

Minimum hit seq length: 0  
 Maximum hit seq length: 200000000  
 Post processing: Minimum Match: 0  
 Maximum Match: 100%

Listing first 45 summaries

Seq ID	Published/Applications/AA*
1	us-09-822-295-15
2	us-09-822-295-15
3	us-09-822-295-15
4	us-09-822-295-15
5	us-09-822-295-15
6	us-09-822-295-15
7	us-09-822-295-15
8	us-09-822-295-15
9	us-09-822-295-15
10	us-09-822-295-15
11	us-09-822-295-15
12	us-09-822-295-15
13	us-09-822-295-15
14	us-09-822-295-15
15	us-09-822-295-15
16	us-09-822-295-15
17	us-09-822-295-15
18	us-09-822-295-15
19	us-09-822-295-15
20	us-09-822-295-15
21	us-09-822-295-15
22	us-09-822-295-15
23	us-09-822-295-15
24	us-09-822-295-15
25	us-09-822-295-15
26	us-09-822-295-15
27	us-09-822-295-15
28	us-09-822-295-15
29	us-09-822-295-15
30	us-09-822-295-15
31	us-09-822-295-15
32	us-09-822-295-15
33	us-09-822-295-15
34	us-09-822-295-15
35	us-09-822-295-15
36	us-09-822-295-15
37	us-09-822-295-15
38	us-09-822-295-15
39	us-09-822-295-15
40	us-09-822-295-15
41	us-09-822-295-15
42	us-09-822-295-15
43	us-09-822-295-15
44	us-09-822-295-15
45	us-09-822-295-15

## ALIGNMENTS

20	49.5	30.0	358	10	US-09-740-027-4	Sequence 4, Appl1
21	49.5	30.0	444	12	US-10-101-841-174	Sequence 170, App
22	49.5	30.0	4551	9	US-09-798-706-1	Sequence 1, Appl1
23	49.5	30.0	4613	9	US-09-860-846-41	Sequence 81, Appl
24	49.5	30.0	4613	9	US-09-948-4848-81	Sequence 81, Appl
25	49.5	30.0	4613	9	US-09-846-821-41	Sequence 81, Appl
26	49.5	30.0	4613	10	US-09-861-289-41	Sequence 81, Appl
27	49.5	30.0	11877	9	US-09-861-289-41	Sequence 81, Appl
28	49.5	30.0	11877	9	US-09-861-289-41	Sequence 81, Appl
29	49.5	30.0	11877	9	US-09-861-289-41	Sequence 81, Appl
30	49.5	30.0	12199	9	US-09-888-3848-6	Sequence 6, Appl1
31	48.5	29.4	85	9	US-09-888-3848-6	Sequence 6, Appl1
32	48.5	29.4	4471	9	US-10-205-032-10	Sequence 1, Appl
33	47	28.5	341	9	US-09-738-626-5637	Sequence 10, Appl
34	47	28.5	970	9	US-10-026-021-2	Sequence 5547, Ap
35	46	27.9	26	9	US-09-813-153-211	Sequence 21, App
36	46	27.9	54	10	US-09-864-761-4837	Sequence 4837, A
37	46	27.9	59	10	US-09-864-761-4837	Sequence 4837, A
38	46	27.9	148	9	US-10-101-464A-823	Sequence 823, App
39	46	27.9	298	9	US-09-812-152-212	Sequence 212, App
40	46	27.9	822	10	US-09-825-561A-82	Sequence 82, App
41	46	27.9	334	9	US-10-023-292-672	Sequence 672, App
42	46	27.9	880	9	US-09-866-052A-678	Sequence 678, App
43	46	27.9	386	9	US-09-211-424-2	Sequence 2, Appl1
44	46	27.9	426	2	US-10-075-528-4	Sequence 4, Appl1
45	46	27.9	729	9	US-10-142-356-11	Sequence 11, Appl

RESULT 1  
 us-09-822-295-15  
 Sequence 15, Appl1  
 Access No. US2001019501A1  
 GENERAL INFORMATION:  
 APPLICANT: Bahija Jallal  
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
 PERIOD RELATED DISORDERS  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENT ADDRESS:  
 ADDRESS: 1500 A 1500  
 SUITE: 934 West 111th Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" diskette, 1.44 MB  
 STORAGE

COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASTSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 15/295,295  
 FILING DATE: 02-Apr-2001  
 CLASSIFICATION: (Unknown)  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: (9708), 445  
 FILING DATE: (Unknown)  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 PREPARATION NUMBER: 72/327  
 REFERENCE/EXCERPT NUMBER: 11/254  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489 1600  
 TELEFAX: (213) 955-0440  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 amino acids

[illegible]

Figure 1. The effect of the *h* parameter on the accuracy of the  $\hat{\mu}_1$  and  $\hat{\mu}_2$  estimators. The figure shows the mean squared error (MSE) of the estimators for different values of  $h$  (0.01, 0.02, 0.05, 0.1, 0.2, 0.5, 1.0, 2.0, 5.0, 10.0, 20.0, 50.0, 100.0, 200.0, 500.0, 1000.0). The MSE generally decreases as  $h$  increases, with the most significant reduction occurring between  $h=0.01$  and  $h=0.1$ . The  $\hat{\mu}_1$  estimator (left) shows a more pronounced decrease in MSE compared to the  $\hat{\mu}_2$  estimator (right).

[illegible][illegible]

1000

[illegible]

REMOVED FROM THE RECORDS OF THE  
OFFICE OF THE ATTORNEY GENERAL  
AUTHORITY: 44 U.S.C. 1904

[illegible]

Methyl benzoate 0.96 M  
Methyl iodide 1.44 M  
Total 1.7

THE UNIVERSITY OF CHICAGO  
 1100 SOUTH EAST ASIAN BLVD.  
 CHICAGO, ILL. 60607-7073  
 TEL: 773/936-5000 FAX: 773/936-5001  
 WWW: WWW.CHICAGO.EDU

\*ACCEPTED FOR PUBLICATION  
 16 JULY 2011  
 ACCEPTED FOR PUBLICATION 16 JULY 2011

NEWARK, N.J. (AP) — The New York City Police Department has announced that it has received information that a man, identified as a member of the Black Liberation Army, is planning to travel to New York City in the near future to carry out a series of bombings.

[illegible][illegible]

M. J. Griffin, School of Mechanical Engineering, The University of Manchester, Oxford Road, Manchester, M13 9PL, England

1. *Method*—The study was a descriptive, cross-sectional survey of 1000 randomly selected, noninstitutionalized, non-Hispanic white, non-Hispanic black, and Mexican American adults living in the community in the Los Angeles area. The study was conducted between 1990 and 1992. The response rate was 70.5%.

[illegible]RESULTS 4  
US 10 102-806-6004

1. FUNDAMENTAL NO. 2200009421A  
2. GENERAL INFORMATION:  
3. CITATION INFORMATION:  
4. ABSTRACT AND KEYWORDS:  
5. AUTHOR INFORMATION:

REGISTERED ATTORNEY FOR ROBERT, 30710/102, 800  
CURRENT FILING DATE: 2002-04-22  
FEDERAL APPLICATION NUMBER: 00/710,236

PERIODICITY DATE: 2000-03-08  
PERIOD APLICATION NUMBER: 60/124, 270  
PERIOD APLICATION DATE: 1999-03-01

SOFTWARD: Patent in Ver. 2.0  
SPO TO NO 606  
LENGTH: 331

```

; POLYNOM: Horro Sadovnik
;
; FEATURE:
; NAME/KEY: STEP
; POSITION: 2018

```

NAME/KEY: SITE  
LOCATION: (285  
OTHER INFORMATION:

## Only Match Best Local Sites

```

cy      1  SMPpSttZSKMStDPlPFXQWtVtPStLP  4
          | | | | | | | | | | | | | | | | | |
td      6) SMTpSttZSKMStDPlPFXQWtVtPStLP  4

```

RES. 11.1 4  
US-00-822-295-1A

PATIENT NO.: 0820020119101M1  
 GENERAL INFORMATION:  
 APPLICANT: Bahija Jallal  
 Giovanni D. Plasmatti

PHOTO RELATED TO SUBJECTS  
NUMBER OF PHOTOSES: 18  
CURRENT ADDRESS:  
CURRENT ADDRESS:

SURREY: 688 West  
 Suite 470  
 City: Los Angeles  
 State: California

ZIP: 94071-2066  
COMPUTER READING ROOM:  
MEDIUM TYPE: 3.5" DISK/100, 1.44 MB

COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM PC, DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0

FILE NO: 02 Apr 2001  
 CLASSIFICATION: Unknown  
 PRIOR APPLICATION DATA:

FILE NO: DATE: UNKNOWN  
ATTORNEY/AGENT INFORMATION:



















© 1993 - 2003 CompuGen Ltd  
 CompuGen version 5.1.6

### Problem statement: using SW mode.

Cell ID	Year	Month	Day	Time	Search time	Updates/second
183.717	2003	12	04	56	6.81319	183.717

```
1: 101      185-07-022-295-.5  
Portlet score:    165  
Sequence:         1 SWPSTGTSKMSIDMLEKODGTVPSSLIP 31
```

See ring table: `bls062`  
`vapor 10.0` , `gapext 0.5`

Seed lot: 112892 seqs, 4476328 residues

Total number of hits satisfying chosen parameters: 112992

Maximum [15 sec] 2000000000

Maximum [15 sec] 2000000000

[illegible][illegible]

## Index and Summary

$$\begin{aligned} \frac{\partial}{\partial t} &= \frac{\partial}{\partial t} + \frac{\partial}{\partial x} \left( \frac{x}{t} \right) = \frac{\partial}{\partial t} + \frac{\partial}{\partial x} \left( \frac{x}{t} \right) \\ &= \frac{\partial}{\partial t} + \frac{\partial}{\partial x} \left( \frac{x}{t} \right) = \frac{\partial}{\partial t} + \frac{\partial}{\partial x} \left( \frac{x}{t} \right) \end{aligned}$$

total. Note that the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Accession No.	Source	GenType	Length	OR	ID	Description
1	148.5	90.0	867	1	PINK_HUMAN	Q9Y372 homo sapiens
2	88.5	93.2	862	1	PTN2_MOUSE	P29352 mus musculus
3	94.0	92.7	319	1	YLX2_BACSU	F50850 bacillus subtilis
4	54	82.1	239	1	FSZ7_MOUSE	F56148 mus musculus
5	54	82.1	339	1	YAP9_SCHPO	O09862 schizosaccharomyces pombe
6	53	82.1	410	1	TRF1_MOUSE	Q09398 neurospora crassa
7	52.5	81.8	476	1	EXL1_TIGAR	Q04211 nicotiana glauca
8	51	81.39	753	1	EMD_KAT	Q09281 rat
9	50.5	80.6	789	1	ARNT_HUMAN	Q63190 rattus norvegicus
10	50.5	80.3	793	1	ARNT_FABIT	F27540 homo sapiens
11	50.5	80.3	793	1	ARNT_MOUSE	Q02748 cyricolagmus
12	50.3	80.2	800	1	ARNT_FAT	F53762 mus musculus
13	49	80.3	1383	1	ARNT_FAT	F41719 rattus norvegicus
14	49	80.3	1477	1	NX1A_CHECK	Q04330 gallus gallus
15	49	80.3	1477	1	NX1A_HUMAN	Q04310 homo sapiens
16	49	80.3	1514	1	NX1A_MOUSE	Q04332 rattus norvegicus
17	49	80.3	1543	1	NX1A_HUMAN	Q04346 bos taurus
18	48.5	79.4	143	1	MM52_MYCTO	Q13736 mycobacterium tuberculosis
19	48	79.4	259	1	EMD_MOUSE	Q08575 mus musculus
20	48	79.4	455	1	YN16_YEAST	P40161 saccharomyces cerevisiae
21	48	79.4	455	1	YN16_YEAST	P12378 bos taurus
22	48	79.4	494	1	U016_ROVIN	Q08340 genome project
23	48	79.4	3683	1	U016_ZYVIR	O06745 arabidopsis thaliana
24	47.5	78.8	374	1	HSP5_AVATH	Q06673 homo sapiens
25	47.5	78.8	381	1	PCN2_HUMAN	Q06672 mus musculus
26	47	78.5	225	1	SP25_MOUSE	P15196 oryzotolagus
27	47	78.5	398	1	S006_KAH11	P36340 venezuelana
28	47	78.5	354	1	PC15_FEYVE	Q06714 drosophila
29	47	78.5	354	1	PC15_FEYVE	Q46844 escherichia coli
30	46	77.9	260	1	KW1_DROME	O06011 homo sapiens
31	46	77.9	386	1	YGH1_ECOLI	P75572 homo sapiens
32	46	77.9	427	1	IFAX_HUMAN	O08888 mus musculus
33	46	77.9	571	1	APR3_MOUSE	P27345 homo sapiens
34	46	77.9	713	1	KP78_HUMAN	Q04341 mus musculus
35	46	77.9	889	1	AKA2_MOUSE	

## APPENDIX IV

## RESULT 1

ID	PTN22_HUMAN	STANDARD:	PTT: 807 AA.
AC	Q9Y063; Q9Y064;		
DE	15-JUN-2002 (Ref. 41), last sequence update)		
DE	15-JUN-2002 (Ref. 41), last annotation update)		
DE	15-JUN-2002 (Ref. 41), last annotation update)		
DE	(Hematopoietic cell protein-tyrosine phosphatase 70Z-PTP) (Tympoid		
DE	phosphatase) (lyt).		
GN	PTN22 OR PTPN22		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_TaxID:9606;		
RN	111		
RP	SEQUENCE FROM N.A. (1991)MEL 1 AND 2) AND CHARACTERIZATION.		
RX	MEL1IN-9916989; PubMed 1046674.		
RA	Cohen S., Dadi H., Shacoul E., Sharda N., Kottman C.M.,		
RI	"Cloning and characterization of a lymphoid specific, inducible human		
RI	protein tyrosine phosphatase, Lyp-2"		
RT	Blood 93:2013-2024(1999).		
RL	121		
RN	SEQUENCE FROM N.A. (ISOFORM 1).		
RP	Liu T., Zhang J., Fu G., Zhang Q., Ye M., Zhou J., Wu J., Shen Y.,		
RA	Yu M., Chen S., Mao M., Chen Z.,		
RI	"Human protein tyrosine phosphatase (70ZPTP) homolog,"		
RI	Submitted (2001-09-09) to the EMBL/GenBank/CCDC databases.		
CC	-1 FUNCTION: Seems to act on Cbl. May play a role in regulating the		
CC	function of Cbl and its associated protein kinases.		
CC	-1 CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H2O = protein		
CC	tyrosine + phosphate.		
CC	-1 SUBCELLULAR LOCATION: Cytoplasmic (by similarity).		
CC	-1 ALTERNATIVE PRODUCTS: 2 isoforms: 1737 (chondrocyte) and 2732		
CC	are produced by alternative splicing.		
CC	-1 TISSUE SPECIFICITY: Predominantly expressed in lymphoid tissues		
CC	and cells. Isoform 1 is expressed in thymocytes and both murine B		
CC	and T cells.		
CC	-1 SIMILARITY: BELONGS TO THE N-N RECEPTOR CLASS OF THE PROTEIN		
CC	TYROSINE PHOSPHATASE FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration between		
CC	the European Bioinformatics Institute (EBI) and the EMBL and has no restriction on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed, altered or used by and for commercial		
CC	purposes.		
CC	-----		
CC	or send an email to <a href="mailto:listserv@ebi.ac.uk">listserv@ebi.ac.uk</a> .		
DR	EMBL: AF001846; AA000904.1;		
DR	EMBL: AF001847; AA000905.1;		
DR	EMBL: AF077031; AA027764.1;		
DR	HSSD: P29350; IGM2		
DR	Genbank: HGNC:9652; PTPN22.		
DR	MIM: 600716.		
DR	InterPro: IPR004595; PTPC_mol1.		





05 Nicotiana glauca (Common tobacco).  
 06 Eukaryotic: Vitis (Grape).  
 07 Spermatophyte: Arabidopsis thaliana (Mustard).  
 08 Astroid: Geranium (Carnation).  
 09 NBI TaxID: 4097.  
 10 NBI TaxID: 4097.  
 11 STRAIN: cv. 'Purpurea'.  
 12 MEDLINE: 93605740; PubMed: 192607.  
 13 Goldstein M.P., Bozard M., Soutnick J., Mariani C.  
 14 "Developmental expression of tobacco pistil specific genes encoding  
 15 novel extensin-like proteins."  
 16 Plant Cell 4:1041-1051 (1992).  
 17 TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).  
 18 DEVELOPMENTAL STAGE: EXPRESSED DURING FLORET BUDS AFTER  
 19 PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING  
 20 FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE  
 21 AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER  
 22 POLLINATION.  
 23 This Swiss-Pro entry is copyright. It is produced through a collaboration  
 24 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 25 at the European Bioinformatics Institute. There are no restrictions on its  
 26 use. It is a public domain entry as far as the copyright is concerned. It may  
 27 be used and then it should be noted that it is not a commercial  
 28 product and that it is not a trademark (see help on how to use it).  
 29 or send an email to: bioinformatics@ebi.ac.uk  
 30 EMBL: 214319; GenBank: U01696.  
 31 PIR: J01696; J01696.  
 32 InterPro: (PROSITE) P01696; P01696.  
 33 PIR: J01696; P01696; P01696.  
 34 Structural protein signal: Repeat: Glycoprotein.  
 35 SIGNAL: 1 24  
 36 CHAIN: 24 426 PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN.  
 37 DOMAIN: 69 182 4 X 5 AA REPEATS OF S104.  
 38 E1: 69 182 4  
 39 E2: 69 182 4  
 40 E3: 69 182 4  
 41 E4: 69 182 4  
 42 E5: 69 182 4  
 43 E6: 69 182 4  
 44 E7: 69 182 4  
 45 E8: 69 182 4  
 46 E9: 69 182 4  
 47 E10: 69 182 4  
 48 E11: 69 182 4  
 49 E12: 69 182 4  
 50 E13: 69 182 4  
 51 E14: 69 182 4  
 52 E15: 69 182 4  
 53 E16: 69 182 4  
 54 E17: 69 182 4  
 55 E18: 69 182 4  
 56 E19: 69 182 4  
 57 E20: 69 182 4  
 58 E21: 69 182 4  
 59 E22: 69 182 4  
 60 E23: 69 182 4  
 61 E24: 69 182 4  
 62 E25: 69 182 4  
 63 E26: 69 182 4  
 64 E27: 69 182 4  
 65 E28: 69 182 4  
 66 E29: 69 182 4  
 67 E30: 69 182 4  
 68 E31: 69 182 4  
 69 E32: 69 182 4  
 70 E33: 69 182 4  
 71 E34: 69 182 4  
 72 E35: 69 182 4  
 73 E36: 69 182 4  
 74 E37: 69 182 4  
 75 E38: 69 182 4  
 76 E39: 69 182 4  
 77 E40: 69 182 4  
 78 E41: 69 182 4  
 79 E42: 69 182 4  
 80 E43: 69 182 4  
 81 E44: 69 182 4  
 82 E45: 69 182 4  
 83 E46: 69 182 4  
 84 E47: 69 182 4  
 85 E48: 69 182 4  
 86 E49: 69 182 4  
 87 E50: 69 182 4  
 88 E51: 69 182 4  
 89 E52: 69 182 4  
 90 E53: 69 182 4  
 91 E54: 69 182 4  
 92 E55: 69 182 4  
 93 E56: 69 182 4  
 94 E57: 69 182 4  
 95 E58: 69 182 4  
 96 E59: 69 182 4  
 97 E60: 69 182 4  
 98 E61: 69 182 4  
 99 E62: 69 182 4  
 100 E63: 69 182 4  
 101 E64: 69 182 4  
 102 E65: 69 182 4  
 103 E66: 69 182 4  
 104 E67: 69 182 4  
 105 E68: 69 182 4  
 106 E69: 69 182 4  
 107 E70: 69 182 4  
 108 E71: 69 182 4  
 109 E72: 69 182 4  
 110 E73: 69 182 4  
 111 E74: 69 182 4  
 112 E75: 69 182 4  
 113 E76: 69 182 4  
 114 E77: 69 182 4  
 115 E78: 69 182 4  
 116 E79: 69 182 4  
 117 E80: 69 182 4  
 118 E81: 69 182 4  
 119 E82: 69 182 4  
 120 E83: 69 182 4  
 121 E84: 69 182 4  
 122 E85: 69 182 4  
 123 E86: 69 182 4  
 124 E87: 69 182 4  
 125 E88: 69 182 4  
 126 E89: 69 182 4  
 127 E90: 69 182 4  
 128 E91: 69 182 4  
 129 E92: 69 182 4  
 130 E93: 69 182 4  
 131 E94: 69 182 4  
 132 E95: 69 182 4  
 133 E96: 69 182 4  
 134 E97: 69 182 4  
 135 E98: 69 182 4  
 136 E99: 69 182 4  
 137 E100: 69 182 4  
 138 E101: 69 182 4  
 139 E102: 69 182 4  
 140 E103: 69 182 4  
 141 E104: 69 182 4  
 142 E105: 69 182 4  
 143 E106: 69 182 4  
 144 E107: 69 182 4  
 145 E108: 69 182 4  
 146 E109: 69 182 4  
 147 E110: 69 182 4  
 148 E111: 69 182 4  
 149 E112: 69 182 4  
 150 E113: 69 182 4  
 151 E114: 69 182 4  
 152 E115: 69 182 4  
 153 E116: 69 182 4  
 154 E117: 69 182 4  
 155 E118: 69 182 4  
 156 E119: 69 182 4  
 157 E120: 69 182 4  
 158 E121: 69 182 4  
 159 E122: 69 182 4  
 160 E123: 69 182 4  
 161 E124: 69 182 4  
 162 E125: 69 182 4  
 163 E126: 69 182 4  
 164 E127: 69 182 4  
 165 E128: 69 182 4  
 166 E129: 69 182 4  
 167 E130: 69 182 4  
 168 E131: 69 182 4  
 169 E132: 69 182 4  
 170 E133: 69 182 4  
 171 E134: 69 182 4  
 172 E135: 69 182 4  
 173 E136: 69 182 4  
 174 E137: 69 182 4  
 175 E138: 69 182 4  
 176 E139: 69 182 4  
 177 E140: 69 182 4  
 178 E141: 69 182 4  
 179 E142: 69 182 4  
 180 E143: 69 182 4  
 181 E144: 69 182 4  
 182 E145: 69 182 4  
 183 E146: 69 182 4  
 184 E147: 69 182 4  
 185 E148: 69 182 4  
 186 E149: 69 182 4  
 187 E150: 69 182 4  
 188 E151: 69 182 4  
 189 E152: 69 182 4  
 190 E153: 69 182 4  
 191 E154: 69 182 4  
 192 E155: 69 182 4  
 193 E156: 69 182 4  
 194 E157: 69 182 4  
 195 E158: 69 182 4  
 196 E159: 69 182 4  
 197 E160: 69 182 4  
 198 E161: 69 182 4  
 199 E162: 69 182 4  
 200 E163: 69 182 4  
 201 E164: 69 182 4  
 202 E165: 69 182 4  
 203 E166: 69 182 4  
 204 E167: 69 182 4  
 205 E168: 69 182 4  
 206 E169: 69 182 4  
 207 E170: 69 182 4  
 208 E171: 69 182 4  
 209 E172: 69 182 4  
 210 E173: 69 182 4  
 211 E174: 69 182 4  
 212 E175: 69 182 4  
 213 E176: 69 182 4  
 214 E177: 69 182 4  
 215 E178: 69 182 4  
 216 E179: 69 182 4  
 217 E180: 69 182 4  
 218 E181: 69 182 4  
 219 E182: 69 182 4  
 220 E183: 69 182 4  
 221 E184: 69 182 4  
 222 E185: 69 182 4  
 223 E186: 69 182 4  
 224 E187: 69 182 4  
 225 E188: 69 182 4  
 226 E189: 69 182 4  
 227 E190: 69 182 4  
 228 E191: 69 182 4  
 229 E192: 69 182 4  
 230 E193: 69 182 4  
 231 E194: 69 182 4  
 232 E195: 69 182 4  
 233 E196: 69 182 4  
 234 E197: 69 182 4  
 235 E198: 69 182 4  
 236 E199: 69 182 4  
 237 E200: 69 182 4  
 238 E201: 69 182 4  
 239 E202: 69 182 4  
 240 E203: 69 182 4  
 241 E204: 69 182 4  
 242 E205: 69 182 4  
 243 E206: 69 182 4  
 244 E207: 69 182 4  
 245 E208: 69 182 4  
 246 E209: 69 182 4  
 247 E210: 69 182 4  
 248 E211: 69 182 4  
 249 E212: 69 182 4  
 250 E213: 69 182 4  
 251 E214: 69 182 4  
 252 E215: 69 182 4  
 253 E216: 69 182 4  
 254 E217: 69 182 4  
 255 E218: 69 182 4  
 256 E219: 69 182 4  
 257 E220: 69 182 4  
 258 E221: 69 182 4  
 259 E222: 69 182 4  
 260 E223: 69 182 4  
 261 E224: 69 182 4  
 262 E225: 69 182 4  
 263 E226: 69 182 4  
 264 E227: 69 182 4  
 265 E228: 69 182 4  
 266 E229: 69 182 4  
 267 E230: 69 182 4  
 268 E231: 69 182 4  
 269 E232: 69 182 4  
 270 E233: 69 182 4  
 271 E234: 69 182 4  
 272 E235: 69 182 4  
 273 E236: 69 182 4  
 274 E237: 69 182 4  
 275 E238: 69 182 4  
 276 E239: 69 182 4  
 277 E240: 69 182 4  
 278 E241: 69 182 4  
 279 E242: 69 182 4  
 280 E243: 69 182 4  
 281 E244: 69 182 4  
 282 E245: 69 182 4  
 283 E246: 69 182 4  
 284 E247: 69 182 4  
 285 E248: 69 182 4  
 286 E249: 69 182 4  
 287 E250: 69 182 4  
 288 E251: 69 182 4  
 289 E252: 69 182 4  
 290 E253: 69 182 4  
 291 E254: 69 182 4  
 292 E255: 69 182 4  
 293 E256: 69 182 4  
 294 E257: 69 182 4  
 295 E258: 69 182 4  
 296 E259: 69 182 4  
 297 E260: 69 182 4  
 298 E261: 69 182 4  
 299 E262: 69 182 4  
 300 E263: 69 182 4  
 301 E264: 69 182 4  
 302 E265: 69 182 4  
 303 E266: 69 182 4  
 304 E267: 69 182 4  
 305 E268: 69 182 4  
 306 E269: 69 182 4  
 307 E270: 69 182 4  
 308 E271: 69 182 4  
 309 E272: 69 182 4  
 310 E273: 69 182 4  
 311 E274: 69 182 4  
 312 E275: 69 182 4  
 313 E276: 69 182 4  
 314 E277: 69 182 4  
 315 E278: 69 182 4  
 316 E279: 69 182 4  
 317 E280: 69 182 4  
 318 E281: 69 182 4  
 319 E282: 69 182 4  
 320 E283: 69 182 4  
 321 E284: 69 182 4  
 322 E285: 69 182 4  
 323 E286: 69 182 4  
 324 E287: 69 182 4  
 325 E288: 69 182 4  
 326 E289: 69 182 4  
 327 E290: 69 182 4  
 328 E291: 69 182 4  
 329 E292: 69 182 4  
 330 E293: 69 182 4  
 331 E294: 69 182 4  
 332 E295: 69 182 4  
 333 E296: 69 182 4  
 334 E297: 69 182 4  
 335 E298: 69 182 4  
 336 E299: 69 182 4  
 337 E300: 69 182 4  
 338 E301: 69 182 4  
 339 E302: 69 182 4  
 340 E303: 69 182 4  
 341 E304: 69 182 4  
 342 E305: 69 182 4  
 343 E306: 69 182 4  
 344 E307: 69 182 4  
 345 E308: 69 182 4  
 346 E309: 69 182 4  
 347 E310: 69 182 4  
 348 E311: 69 182 4  
 349 E312: 69 182 4  
 350 E313: 69 182 4  
 351 E314: 69 182 4  
 352 E315: 69 182 4  
 353 E316: 69 182 4  
 354 E317: 69 182 4  
 355 E318: 69 182 4  
 356 E319: 69 182 4  
 357 E320: 69 182 4  
 358 E321: 69 182 4  
 359 E322: 69 182 4  
 360 E323: 69 182 4  
 361 E324: 69 182 4  
 362 E325: 69 182 4  
 363 E326: 69 182 4  
 364 E327: 69 182 4  
 365 E328: 69 182 4  
 366 E329: 69 182 4  
 367 E330: 69 182 4  
 368 E331: 69 182 4  
 369 E332: 69 182 4  
 370 E333: 69 182 4  
 371 E334: 69 182 4  
 372 E335: 69 182 4  
 373 E336: 69 182 4  
 374 E337: 69 182 4  
 375 E338: 69 182 4  
 376 E339: 69 182 4  
 377 E340: 69 182 4  
 378 E341: 69 182 4  
 379 E342: 69 182 4  
 380 E343: 69 182 4  
 381 E344: 69 182 4  
 382 E345: 69 182 4  
 383 E346: 69 182 4  
 384 E347: 69 182 4  
 385 E348: 69 182 4  
 386 E349: 69 182 4  
 387 E350: 69 182 4  
 388 E351: 69 182 4  
 389 E352: 69 182 4  
 390 E353: 69 182 4  
 391 E354: 69 182 4  
 392 E355: 69 182 4  
 393 E356: 69 182 4  
 394 E357: 69 182 4  
 395 E358: 69 182 4  
 396 E359: 69 182 4  
 397 E360: 69 182 4  
 398 E361: 69 182 4  
 399 E362: 69 182 4  
 400 E363: 69 182 4  
 401 E364: 69 182 4  
 402 E365: 69 182 4  
 403 E366: 69 182 4  
 404 E367: 69 182 4  
 405 E368: 69 182 4  
 406 E369: 69 182 4  
 407 E370: 69 182 4  
 408 E371: 69 182 4  
 409 E372: 69 182 4  
 410 E373: 69 182 4  
 411 E374: 69 182 4  
 412 E375: 69 182 4  
 413 E376: 69 182 4  
 414 E377: 69 182 4  
 415 E378: 69 182 4  
 416 E379: 69 182 4  
 417 E380: 69 182 4  
 418 E381: 69 182 4  
 419 E382: 69 182 4  
 420 E383: 69 182 4  
 421 E384: 69 182 4  
 422 E385: 69 182 4  
 423 E386: 69 182 4  
 424 E387: 69 182 4  
 425 E388: 69 182 4  
 426 E389: 69 182 4  
 427 E390: 69 182 4  
 428 E391: 69 182 4  
 429 E392: 69 182 4  
 430 E393: 69 182 4  
 431 E394: 69 182 4  
 432 E395: 69 182 4  
 433 E396: 69 182 4  
 434 E397: 69 182 4  
 435 E398: 69 182 4  
 436 E399: 69 182 4  
 437 E400: 69 182 4  
 438 E401: 69 182 4  
 439 E402: 69 182 4  
 440 E403: 69 182 4  
 441 E404: 69 182 4  
 442 E405: 69 182 4  
 443 E406: 69 182 4  
 444 E407: 69 182 4  
 445 E408: 69 182 4  
 446 E409: 69 182 4  
 447 E410: 69 182 4  
 448 E411: 69 182 4  
 449 E412: 69 182 4  
 450 E413: 69 182 4  
 451 E414: 69 182 4  
 452 E415: 69 182 4  
 453 E416: 69 182 4  
 454 E417: 69 182 4  
 455 E418: 69 182 4  
 456 E419: 69 182 4  
 457 E420: 69 182 4  
 458 E421: 69 182 4  
 459 E422: 69 182 4  
 460 E423: 69 182 4  
 461 E424: 69 182 4  
 462 E425: 69 182 4  
 463 E426: 69 182 4  
 464 E427: 69 182 4  
 465 E428: 69 182 4  
 466 E429: 69 182 4  
 467 E430: 69 182 4  
 468 E431: 69 182 4  
 469 E432: 69 182 4  
 470 E433: 69 182 4  
 471 E434: 69 182 4  
 472 E435: 69 182 4  
 473 E436: 69 182 4  
 474 E437: 69 182 4  
 475 E438: 69 182 4  
 476 E439: 69 182 4  
 477 E440: 69 182 4  
 478 E441: 69 182 4  
 479 E442: 69 182 4  
 480 E443: 69 182 4  
 481 E444: 69 182 4  
 482 E445: 69 182 4  
 483 E446: 69 182 4  
 484 E447: 69 182 4  
 485 E448: 69 182 4  
 486 E449: 69 182 4  
 487 E450: 69 182 4  
 488 E451: 69 182 4  
 489 E452: 69 182 4  
 490 E453: 69 182 4  
 491 E454: 69 182 4  
 492 E455: 69 182 4  
 493 E456: 69 182 4  
 494 E457: 69 182 4  
 495 E458: 69 182 4  
 496 E459: 69 182 4  
 497 E460: 69 182 4  
 498 E461: 69 182 4  
 499 E462: 69 182 4  
 500 E463: 69 182 4  
 501 E464: 69 182 4  
 502 E465: 69 182 4  
 503 E466: 69 182 4  
 504 E467: 69 182 4  
 505 E468: 69 182 4  
 506 E469: 69 182 4  
 507 E470: 69 182 4  
 508 E471: 69 182 4  
 509 E472: 69 182 4  
 510 E473: 69 182 4  
 511 E474: 69 182 4  
 512 E475: 69 182 4  
 513 E476: 69 182 4  
 514 E477: 69 182 4  
 515 E478: 69 182 4  
 516 E479: 69 182 4  
 517 E480: 69 182 4  
 518 E481: 69 182 4  
 519 E482: 69 182 4  
 520 E483: 69 182 4  
 521 E484: 69 182 4  
 522 E485: 69 182 4  
 523 E486: 69 182 4  
 524 E487: 69 182 4  
 525 E488: 69 182 4  
 526 E489: 69 182 4  
 527 E490: 69 182 4  
 528 E491: 69 182 4  
 529 E492: 69 182 4  
 530 E493: 69 182 4  
 531 E494: 69 182 4  
 532 E495: 69 182 4  
 533 E496: 69 182 4  
 534 E497: 69 182 4  
 535 E498: 69 182 4  
 536 E499: 69 182 4  
 537 E500: 69 182 4  
 538 E501: 69 182 4  
 539 E502: 69 182 4  
 540 E503: 69 182 4  
 541 E504: 69 182 4  
 542 E505: 69 182 4  
 543 E506: 69 182 4  
 544 E507: 69 182 4  
 545 E508: 69 182 4  
 546 E509: 69 182 4  
 547 E510: 69 182 4  
 548 E511: 69 182 4  
 549 E512: 69 182 4  
 550 E513: 69 182 4  
 551 E514: 69 182 4  
 552 E515: 69 182 4  
 553 E516: 69 182 4  
 554 E517: 69 182 4  
 555 E518: 69 182 4  
 556 E519: 69 182 4  
 557 E520: 69 182 4  
 558 E521: 69 182 4  
 559 E522: 69 182 4  
 560 E523: 69 182 4  
 561 E524: 69 182 4  
 562 E525: 69 182 4  
 563 E526: 69 182 4  
 564 E527: 69 182 4  
 565 E528: 69 182 4  
 566 E529: 69 182 4  
 567 E530: 69 182 4











NORTHAMERICAN PRECURSOR (Neurexin I-Alpha) -  
NEMO, neurexins (Katz),  
FISH AND MOLLUSCS (Chabala; Vertebrata: Putelesomus;  
Mollusca: Liliidae; Kudo et al.; Sclerozoophora; Muridae; Rattus

CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions or for non-commercial purposes.



Core version 5.1.6  
Copyright © 1994 - 2003 CompuGen Ltd.

Copyright © 1993 - 2003 CompuGen Ltd.

## Model selection using sw model

Search time 24.5275 seconds  
(without alignments)

(without alignments)

260.421 Million cell updates/sec

1-800-822-2455

```
Sequence: SWTOSTSKMSLDLPKQJWVPSSLIP 31
```

```
Sequence: SWTOSTSKMSLDLPKQJWVPSSLIP 31
```

$$S^{\infty} \times \mathbb{R}^n \rightarrow \mathbb{R}^n, \quad (x, t) \mapsto S^{\infty} \times \mathbb{R}^n$$

output 10.0 , deposit 0.5

20604715 residues

Number of hits satisfying chosen parameters: 671583

[illegible]

# Mathematical Analysis

Year	First Round	Second Round	Third Round	Fourth Round	Final
1997	1997-98	1998-99	1999-00	2000-01	2001-02
1998	1998-99	1999-00	2000-01	2001-02	2002-03
1999	1999-00	2000-01	2001-02	2002-03	2003-04
2000	2000-01	2001-02	2002-03	2003-04	2004-05
2001	2001-02	2002-03	2003-04	2004-05	2005-06
2002	2002-03	2003-04	2004-05	2005-06	2006-07
2003	2003-04	2004-05	2005-06	2006-07	2007-08
2004	2004-05	2005-06	2006-07	2007-08	2008-09
2005	2005-06	2006-07	2007-08	2008-09	2009-10
2006	2006-07	2007-08	2008-09	2009-10	2010-11
2007	2007-08	2008-09	2009-10	2010-11	2011-12
2008	2008-09	2009-10	2010-11	2011-12	2012-13
2009	2009-10	2010-11	2011-12	2012-13	2013-14
2010	2010-11	2011-12	2012-13	2013-14	2014-15
2011	2011-12	2012-13	2013-14	2014-15	2015-16
2012	2012-13	2013-14	2014-15	2015-16	2016-17
2013	2013-14	2014-15	2015-16	2016-17	2017-18
2014	2014-15	2015-16	2016-17	2017-18	2018-19
2015	2015-16	2016-17	2017-18	2018-19	2019-20
2016	2016-17	2017-18	2018-19	2019-20	2020-21
2017	2017-18	2018-19	2019-20	2020-21	2021-22
2018	2018-19	2019-20	2020-21	2021-22	2022-23
2019	2019-20	2020-21	2021-22	2022-23	2023-24
2020	2020-21	2021-22	2022-23	2023-24	2024-25
2021	2021-22	2022-23	2023-24	2024-25	2025-26
2022	2022-23	2023-24	2024-25	2025-26	2026-27
2023	2023-24	2024-25	2025-26	2026-27	2027-28
2024	2024-25	2025-26	2026-27	2027-28	2028-29
2025	2025-26	2026-27	2027-28	2028-29	2029-30
2026	2026-27	2027-28	2028-29	2029-30	2030-31
2027	2027-28	2028-29	2029-30	2030-31	2031-32
2028	2028-29	2029-30	2030-31	2031-32	2032-33
2029	2029-30	2030-31	2031-32	2032-33	2033-34
2030	2030-31	2031-32	2032-33	2033-34	2034-35
2031	2031-32	2032-33	2033-34	2034-35	2035-36
2032	2032-33	2033-34	2034-35	2035-36	2036-37
2033	2033-34	2034-35	2035-36	2036-37	2037-38
2034	2034-35	2035-36	2036-37	2037-38	2038-39
2035	2035-36	2036-37	2037-38	2038-39	2039-40
2036	2036-37	2037-38	2038-39	2039-40	2040-41
2037	2037-38	2038-39	2039-40	2040-41	2041-42
2038	2038-39	2039-40	2040-41	2041-42	2042-43
2039	2039-40	2040-41	2041-42	2042-43	2043-44
2040	2040-41	2041-42	2042-43	2043-44	2044-45
2041	2041-42	2042-43	2043-44	2044-45	2045-46
2042	2042-43	2043-44	2044-45	2045-46	2046-47
2043	2043-44	2044-45	2045-46	2046-47	2047-48
2044	2044-45	2045-46	2046-47	2047-48	2048-49
2045	2045-46	2046-47	2047-48	2048-49	2049-50
2046					

[illegible][illegible][illegible][illegible][illegible][illegible][illegible]

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

[illegible]

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

[illegible]

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

[illegible]

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_mammal.*
6: sp_neurocrustator.*
7: sp_plant.*
8: sp_rhizome.*
9: sp_scholaria.*
10: sp_shrub.*
11: sp_plant.*
12: sp_podiat.*
13: sp_virus.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_mycetozoa.*
17: sp_microcyp.*

```

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

```

101: 17: sp_algaey: *
102: 16: sp_bacteria: *
103: 15: sp_fungi: *
104: 14: sp_insect: *
105: 13: sp_mammal: *
106: 12: sp_plant: *
107: 11: sp_reptile: *
108: 10: sp_vertebrate: *
109: 9: sp_worm: *
110: 8: sp_invertebrate: *
111: 7: sp_mollusk: *
112: 6: sp_fish: *
113: 5: sp_arthropod: *
114: 4: sp_mammal: *
115: 3: sp_insect: *
116: 2: sp_plant: *
117: 1: sp_algaey: *

```

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

```

SOLIMBIO_21.*
1: sp_algae.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_insect.*
5: sp_herbivore.*
6: sp_heterotroph.*
7: sp_mammal.*
8: sp_rabbit.*
9: sp_reptile.*
10: sp_plant.*
11: sp_podiat.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_worm.*
16: sp_carnivore.*
17: sp_decapod.*

```

Proof. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARY

Accession	Strain	Genotype	Length	DB	ID	Description
1	148-5	90-0	795	4	Q9P002	Q9P002 homo sapien
2	67	40-6	807	11	Q9Y59	Q9Y59 mus musculu
3	61	37-0	652	4	Q9H94	Q9H94 homo sapien
4	59-1	30-0	654	5	Q1Y284	Q1Y284 caenorhabdi
5	66	43-3	819	11	Q9SVZ7	Q9SVZ7 arabisopsis
6	65	33-3	863	11	Q9C5E7	Q9C5E7 arabidopsis
7	64	42-1	816	13	Q9RSV4	Q9RSV4 tetrahirus t
8	62	41-5	281	19	Q9Z2K4	Q9Z2K4 rhizobium r
9	62	41-5	484	11	Q48967	Q48967 zeamays (n
10	61	42-5	436	19	Q9RTX6	Q9RTX6 deimococcu
11	61	42-9	293	12	Q85078	Q85078 poa semilla
12	61	42-7	260	2	Q88055	Q88055 rhizoclia m
13	61	43-3	1158	16	Q9Y120	Q9Y120 brucecia m
14	61	39-9	2152	10	Q9SN01	Q9SN01 arabidopsis
15	61	41-6	151	15	Q1Z387	Q1Z387 streptomyce
16	50-5	40-6	182	2	Q9H007	Q9H007 streptomyce

## ALLEGEMENTS

17	50.5	30.6	197	4	Q55RM4	bus - Lantus
18	50.5	30.6	730	4	Q48P72	vehicle - bus - Lantus
19	50.5	30.6	791	11	Q52T1F3	vehicle - bus - mus - Lantus
20	50.5	30.6	1692	5	Q5NKA5	vehicle - Lantus - mus - Lantus
21	50	30.3	264	5	Q170U4	Q170U4 - Lantus - Lantus
22	50	30.3	265	10	Q88CV7	Q88CV7 - Lantus - Lantus
23	50	30.3	475	10	Q68L17	Q68L17 - Lantus - Lantus
24	50	30.3	545	5	Q5R017	Q5R017 - Lantus - Lantus
25	49.5	30.0	538	4	Q14745	Q14745 - Lantus - Lantus
26	49.5	30.0	1366	4	Q914W5	Q914W5 - Lantus - Lantus
27	49.5	30.0	4613	2	Q82X15	Q82X15 - Lantus - Lantus
28	49	29.7	214	17	Q8TMC5	Q8TMC5 - Lantus - Lantus
29	49	29.7	258	10	Q498B7	Q498B7 - Lantus - Lantus
30	49	29.7	322	16	Q915B4	Q915B4 - Lantus - Lantus
31	49	29.7	405	17	Q59X17	Q59X17 - Lantus - Lantus
32	46	29.7	856	10	Q9RA11	Q9RA11 - Lantus - Lantus
33	49	29.7	986	10	Q94E10	Q94E10 - Lantus - Lantus
34	49	29.7	1073	10	Q6SEV0	Q6SEV0 - Lantus - Lantus
35	48.5	29.4	207	5	Q88J28	Q88J28 - Lantus - Lantus
36	48.5	29.4	337	4	Q9H577	Q9H577 - Lantus - Lantus
37	48.5	29.4	358	6	Q2R619	Q2R619 - Lantus - Lantus
38	48.5	29.4	530	10	Q94CT0	Q94CT0 - Lantus - Lantus
39	48.5	29.4	706	16	Q59P20	Q59P20 - Lantus - Lantus
40	48.5	29.4	804	10	Q91X73	Q91X73 - Lantus - Lantus
41	48	29.1	256	16	Q8XK81	Q8XK81 - Lantus - Lantus
42	48	29.1	267	10	Q97EYA	Q97EYA - Lantus - Lantus
43	48	29.1	269	10	Q905K1	Q905K1 - Lantus - Lantus
44	48	29.1	300	16	Q97R04	Q97R04 - Lantus - Lantus
45	48	29.1	375	10	Q97041	Q97041 - Lantus - Lantus

## RESULT

```

Q9P002
1D Q9P002 PRELIMINARY; PRT: 799 AA.
AC Q9P002:
DE 01-OCT-2000 (TREMBLREL, 15, created)
FE 01-OCT-2000 (TREMBLREL, 15, last sequence update)
DE 01-JUN-2002 (TREMBLREL, 21, last annotation update)
DE Protein tyrosine phosphatase,
PTP.
CS Homo sapiens (Human).
CC Pukaryotae; Metazoa; Chordata; Craniata; Vertebrata; Teleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RA Huang C., Zhang C., Wu P., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,
RA Han Z., Wang Y., Chen Z., Fu G.;
RT "A novel gene expressed in human adrenal gland.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF150732; AACF67472.1;
DR HSSP: P29350; 1GWZ.
DE InterPro: IPR003387; TYR_phosphatase.
DE InterPro: IPR002422; PTP_Pp.
DE Pfam: PF00102; Y_Phasphatase_1.
DE PRINTS: PR00700; PRTYPTPHASE.
DR SMART: SM00194; PTPc_1.
DE PROSITE: PS00483; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DE PROSITE: PS50055; TYR_PHOSPHATASE_PTP_1.
KW Hydroxylase.
SQ SEQUENCE 799 AA; 90610 MW; 9435485016F34D0C CRC64;

Query Match 90.0%; Score 148.5; E# 4; Length 799;
Post Local Similarity 56.8%; Prot. No. 7460132;
Matches 30; Conservative 0; Mismatch 0; Indels 12; Gaps 1

```



















11. The protein is a member of the ALK-7 (also known as type 1 receptor  
 12. tyrosine kinase) family, known to promote protein survival,  
 13. particularly in the context of hematopoietic progenitors and hematopoiesis.  
 14. The protein is a member of the phosphatase class of the  
 15. protein tyrosine kinase family and is a member of the  
 16. protein tyrosine kinase family. The protein is a member of the  
 17. protein tyrosine kinase family and is a member of the  
 18. protein tyrosine kinase family. The protein is a member of the  
 19. protein tyrosine kinase family and is a member of the  
 20. protein tyrosine kinase family. The protein is a member of the  
 21. protein tyrosine kinase family and is a member of the  
 22. protein tyrosine kinase family. The protein is a member of the  
 23. protein tyrosine kinase family and is a member of the  
 24. protein tyrosine kinase family. The protein is a member of the  
 25. protein tyrosine kinase family and is a member of the  
 26. protein tyrosine kinase family. The protein is a member of the  
 27. protein tyrosine kinase family and is a member of the  
 28. protein tyrosine kinase family. The protein is a member of the  
 29. protein tyrosine kinase family and is a member of the  
 30. protein tyrosine kinase family. The protein is a member of the  
 31. protein tyrosine kinase family and is a member of the  
 32. protein tyrosine kinase family. The protein is a member of the  
 33. protein tyrosine kinase family and is a member of the  
 34. protein tyrosine kinase family. The protein is a member of the  
 35. protein tyrosine kinase family and is a member of the  
 36. protein tyrosine kinase family. The protein is a member of the  
 37. protein tyrosine kinase family and is a member of the  
 38. protein tyrosine kinase family. The protein is a member of the  
 39. protein tyrosine kinase family and is a member of the  
 40. protein tyrosine kinase family. The protein is a member of the  
 41. protein tyrosine kinase family and is a member of the  
 42. protein tyrosine kinase family. The protein is a member of the  
 43. protein tyrosine kinase family and is a member of the  
 44. protein tyrosine kinase family. The protein is a member of the  
 45. protein tyrosine kinase family and is a member of the  
 46. protein tyrosine kinase family. The protein is a member of the  
 47. protein tyrosine kinase family and is a member of the  
 48. protein tyrosine kinase family. The protein is a member of the  
 49. protein tyrosine kinase family and is a member of the  
 50. protein tyrosine kinase family. The protein is a member of the  
 51. protein tyrosine kinase family and is a member of the  
 52. protein tyrosine kinase family. The protein is a member of the  
 53. protein tyrosine kinase family and is a member of the  
 54. protein tyrosine kinase family. The protein is a member of the  
 55. protein tyrosine kinase family and is a member of the  
 56. protein tyrosine kinase family. The protein is a member of the  
 57. protein tyrosine kinase family and is a member of the  
 58. protein tyrosine kinase family. The protein is a member of the  
 59. protein tyrosine kinase family and is a member of the  
 60. protein tyrosine kinase family. The protein is a member of the  
 61. protein tyrosine kinase family and is a member of the  
 62. protein tyrosine kinase family. The protein is a member of the  
 63. protein tyrosine kinase family and is a member of the  
 64. protein tyrosine kinase family. The protein is a member of the  
 65. protein tyrosine kinase family and is a member of the  
 66. protein tyrosine kinase family. The protein is a member of the  
 67. protein tyrosine kinase family and is a member of the  
 68. protein tyrosine kinase family. The protein is a member of the  
 69. protein tyrosine kinase family and is a member of the  
 70. protein tyrosine kinase family. The protein is a member of the  
 71. protein tyrosine kinase family and is a member of the  
 72. protein tyrosine kinase family. The protein is a member of the  
 73. protein tyrosine kinase family and is a member of the  
 74. protein tyrosine kinase family. The protein is a member of the  
 75. protein tyrosine kinase family and is a member of the  
 76. protein tyrosine kinase family. The protein is a member of the  
 77. protein tyrosine kinase family and is a member of the  
 78. protein tyrosine kinase family. The protein is a member of the  
 79. protein tyrosine kinase family and is a member of the  
 80. protein tyrosine kinase family. The protein is a member of the  
 81. protein tyrosine kinase family and is a member of the  
 82. protein tyrosine kinase family. The protein is a member of the  
 83. protein tyrosine kinase family and is a member of the  
 84. protein tyrosine kinase family. The protein is a member of the  
 85. protein tyrosine kinase family and is a member of the  
 86. protein tyrosine kinase family. The protein is a member of the  
 87. protein tyrosine kinase family and is a member of the  
 88. protein tyrosine kinase family. The protein is a member of the  
 89. protein tyrosine kinase family and is a member of the  
 90. protein tyrosine kinase family. The protein is a member of the  
 91. protein tyrosine kinase family and is a member of the  
 92. protein tyrosine kinase family. The protein is a member of the  
 93. protein tyrosine kinase family and is a member of the  
 94. protein tyrosine kinase family. The protein is a member of the  
 95. protein tyrosine kinase family and is a member of the  
 96. protein tyrosine kinase family. The protein is a member of the  
 97. protein tyrosine kinase family and is a member of the  
 98. protein tyrosine kinase family. The protein is a member of the  
 99. protein tyrosine kinase family and is a member of the  
 100. protein tyrosine kinase family. The protein is a member of the

101. (BSC-1) HSC RES & DEV LPL  
 102. Kollman CM  
 103. WPL: 1999 444304/47  
 104. N-PSD: AAX00695  
 105. New nucleic acid encoding intracellular tyrosine phosphatase and  
 106. related proteins, used to mediate signaling through T cells;  
 107. particularly as immunosuppressant  
 108. claim 4a: page 54: 105pp: English  
 109. The present protein sequence is that of the cytoplasmic lymphoid  
 110. protein tyrosine phosphatase Lyp1, that has a single catalytic domain.  
 111. The non-catalytic portion of the phosphatase contains unique sequences,  
 112. including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr.  
 113. Lyp1 is expressed in the lymphoid cells, particularly in T-lymphocytes,  
 114. mature B and T cells and expression is increased upon activation.  
 115. It is involved in lymphocyte growth and development and is  
 116. phosphorylated in a cell cycle dependent manner. Lyp1 shares about 70%  
 117. sequence identity with the murine phosphatase Z70ppp. Lyp proteins are  
 118. important for regulation of T cell antigen and cytokine receptor  
 119. signaling and for early and late stages of T cell differentiation. Lyp1  
 120. has immunosuppressive activity, compounds that increase expression of  
 121. Lyp protein can be used as immunosuppressive agents to reduce or prevent  
 122. T cell activation or proliferation, to control lymphocyte differentiation  
 123. and to treat autoimmune diseases and transplant situations.  
 124. Sequence: 808 AA:  
 125. Query Match: 100.0%, Score: 161, 28, 20, Length: 808  
 126. Best Local Similarity: 100.0%, Field: No. 5, 16-16  
 127. Matching: 79, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0  
 128. I YSLA YPSKRLH LKASWKRHHLSALVYSY 529  
 129. 500 YSLA YPSKRLH LKASWKRHHLSALVYSY 529  
 130. RESULT 7  
 131. ID: AAW38456 standard: Protein: 459 AA  
 132. AAW38456:  
 133. 08 JUN 1998 (first entry)  
 134. Solizosaccharomyces pombe RNA-binding protein ZPR1.  
 135. ZPR1: RNA binding protein, non-activated receptor complex;  
 136. yeast signal transduction; epidermal growth factor receptor;  
 137. pleiotropic growth factor receptor; receptor; marker;  
 138. antibodies; S2 diabetic rat insulin; fibronectin; arthritis;  
 139. proteinase; extrinsic; atrophic; renal; failure; therapy;  
 140. Solizosaccharomyces pombe.  
 141. Key: Location/Qualifiers  
 142. Domain: 37-70  
 143. Domain: 259-291  
 144. Domain: 291-310  
 145. W09/46684 A1.  
 146. 11 Dec 1997.  
 147. 06 JUN 1997: 9706-058991.  
 148. 06 JUN 1996: 9608 0019219.  
 149. (HYMA ) GENBANK:U05818.  
 150.









XX (i) and (ii) are used for the development of vaccines against P. falciparum infection. (1) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (1); are used; in the detection of infection with P. falciparum. Furthermore, (1) (especially when they are in the form of secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAG70078 to AAG70287 and AAB70144 to AAB70452 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.

XX Sequence 2485 AA:

XX Query Match 60.4%, Score 59, BH 21, Length 2485;

XX Best Local Similarity 54.78%, Prot. No. 4 B0102, 00 Caps 0;

XX Ratios 87 Conservative 57 Mismatches 27 Indels 00 Caps 0;

XX 1: 1111111111

XX 13: 170 DNRGDRSSNVQHY 184

XX

XX RESULT 15

XX AAG18984

XX ID AAG18984 standard; Protein; 222 AA.

XX

XX AAG18984:

XX

XX 18-FEB-2002 (first entry)

XX

XX Novel human diagnostic protein #18975.

XX

XX Human chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder;

XX

XX Homo sapiens.

XX

XX M0200175067 A2.

XX

XX 11-oct-2001.

XX

XX 40 MAR 2001: 2501W0 US08061.

XX

XX 31 MAR 2000: 2000W0 0540217.

XX

XX 24 AUG 2000: 2000ZS 0649167.

XX

XX (HYTE ) HYTEG INC.

XX

XX Diagnostic RT, Liu C, Tang YF;

XX

XX WPI: 2001-639662/74.

XX

XX N PSHG AASH4171.

XX

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnosis; forensic; gene mapping; identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity

XX

XX Claim 20; SEQ ID No 4044; 104PP; English.

XX

XX The present invention relates to isolated polynucleotide (1) and

XX polypeptide (ii) sequences, (1) is useful as hybridisation probes,

XX polynucleotide chain reaction (PCR) primers, oligonucleotides, and

XX and gene mapping, and in recombinant production of (1). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (1) is useful in gene therapy techniques

XX (i) and (ii) are used for the development of vaccines against P. falciparum infection. (1) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (1); are used; in the detection of infection with P. falciparum. Furthermore, (1) (especially when they are in the form of secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAG70078 to AAG70287 and AAB70144 to AAB70452 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.

XX Sequence 2485 AA:

XX Query Match 60.4%, Score 59, BH 21, Length 2485;

XX Best Local Similarity 54.78%, Prot. No. 4 B0102, 00 Caps 0;

XX Ratios 87 Conservative 57 Mismatches 27 Indels 00 Caps 0;

XX 1: 1111111111

XX 13: 170 DNRGDRSSNVQHY 184

XX

XX RESULT 15

XX AAG18984

XX ID AAG18984 standard; Protein; 222 AA.

XX

XX AAG18984:

XX

XX 18-FEB-2002 (first entry)

XX

XX Novel human diagnostic protein #18975.

XX

XX Human chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder;

XX

XX Homo sapiens.

XX

XX M0200175067 A2.

XX

XX 11-oct-2001.

XX

XX 40 MAR 2001: 2501W0 US08061.

XX

XX 31 MAR 2000: 2000W0 0540217.

XX

XX 24 AUG 2000: 2000ZS 0649167.

XX

XX (HYTE ) HYTEG INC.

XX

XX Diagnostic RT, Liu C, Tang YF;

XX

XX WPI: 2001-639662/74.

XX

XX N PSHG AASH4171.

XX

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnosis; forensic; gene mapping; identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity

XX

XX Claim 20; SEQ ID No 4044; 104PP; English.

XX

XX The present invention relates to isolated polynucleotide (1) and

XX polypeptide (ii) sequences, (1) is useful as hybridisation probes,

XX polynucleotide chain reaction (PCR) primers, oligonucleotides, and

XX and gene mapping, and in recombinant production of (1). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (1) is useful in gene therapy techniques

to restore normal activity of (1) or to treat disease states involving (1); (1) is useful for generating antibodies against it; detecting or identifying a polypeptide in tissue, as molecular weight markers and as a food supplement; (1) and its binding partners are useful in medical testing of stress expression; (1); (1) and (1) are useful for treating fibrosis involving aberrant protein expression or biological activity; the polypeptide and polynucleotide sequences have applications in diagnostics; forensics; gene mapping; identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to provide other types of data and products dependent on DNA and amino acid sequences; Ab00010-Ab03077 represent novel human fibronectin amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/published\\_fcl\\_sequences](http://wipo.int/pub/published_fcl_sequences).

XX Sequence: 22: AA:

Query: March 24: 89; Score 48; DB 22; Length 222;

Best local Similarity 45: 24; Pred. No: 32;

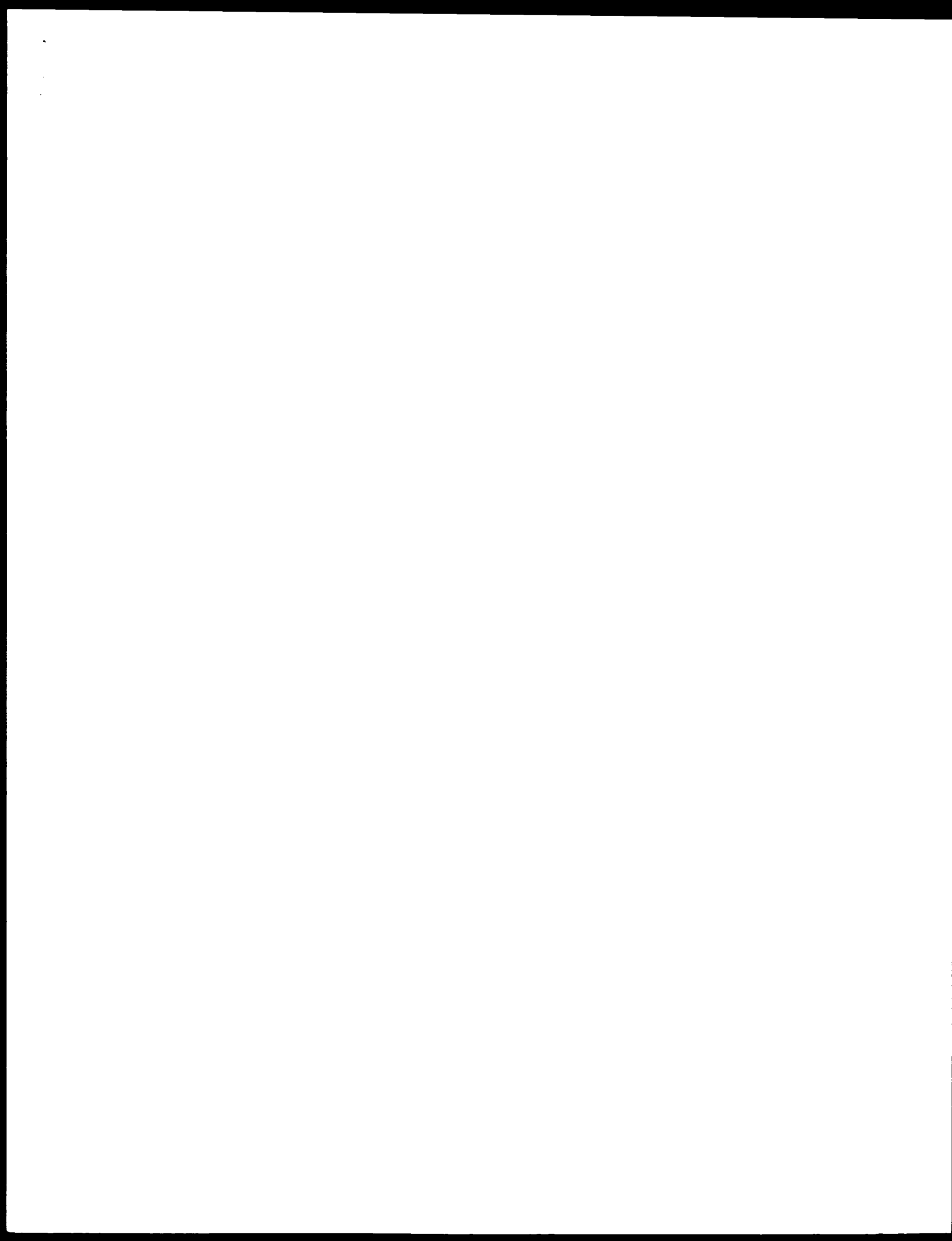
Motif: 14: Conservative 2; Mismatches 11; Indels 4; Gaps 2;

QY 4 LEVSK-HQIRNASNKH-HDSALGVYS 29

111 11 21 1 011111

24 92 LLYRNMYHAFIASTARHYVNSALGVCS 122

Search completed: July 8, 2003 12:09:47  
Total time: 1:01:44:58





[illegible]

```

1 NUMBER OF SEQUENCES: 45
2
3 CORRESPONDENT ADDRESS:
4 ADDRESSEE: FISH & Richardson P.O.
5 STREET: 225 Franklin Street
6 CITY: Boston
7 STATE: MA
8 COUNTRY: US
9 ZIP: 02110-2804
10
11 COMPUTER READABLE FORM:
12 METHOD TYPE: FISHNET
13
14 OPERATING SYSTEM: Windows95
15 SOFTWARE: FASTSEQ for Windows Version 2.3
16
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/04/870,513
19 FILING DATE: 06 JUN 1997
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 60/019,219
23 FILING DATE: 06 JUN 1996
24
25 ATTORNEY/AGENT INFORMATION:
26 NAME: FASSO, Peter J.
27 REGISTRATION NUMBER: 32,983
28 REGISTRY/REGISTER NUMBER: 10209/102001
29
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 617/542-6070
32 TELEFAX: 617/542-8906
33
34 TELEX: 200154
35
36 INFORMATION FOR SEQ ID NO: 4:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 459 amino acids
39 TYPE: amino acid
40
41 TOPOLOGY: linear
42
43 MOLECULE TYPE: protein
44
45 US-04-870-513-4
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976

```

US 9,410,464 B2  
 2. Priority 12. Application US/9410464  
 3. Filed Nov. 6, 1992  
 4. REFERENCE INFORMATION  
 5. APPLICANT: SINGH, et al.  
 6. TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering time  
 7. FIELD OF INVENTION: floral and other plant species.  
 8. FILE REFERENCE: 53375  
 9. CURRENT APPLICANT: SINGH, et al. 9,410,464  
 10. PREVIOUS APPLICANT: SINGH, et al. 9,410,464  
 11. EARLIER APPLICANT: SINGH, et al. 9,410,464  
 12. EARLIER FILING DATE: 1999-04-06  
 13. EARLIER APPLICATION NUMBER: 9,410,464

REFERENCE/DOCKET NUMBER: PF-0410 02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
GI: 561632  
OS: 08-869-733-3

Query Match	28.0%	Score 37	19.2	Length 120
Best Local Similarity	43.8%			
Matches	7	Conservative	5	Mismatches
			4	Indels
			0	Gaps
Q9	5	ESKESLRNAYVKKND	21	
	111	: : : : 15 : 11		
D3	90	DSKVEVNNINNNINND	105	





```

1  INFO: INFORMATION INFORMATION:
2  TELEPHONE: 415-845-0555
3  TELEFAX: 415-845-4156
4  SUBJECT: unknown
5  INFORMATION IN SEQ ID NO: 4:
6  SEQUENCE CHARACTERISTICS:
7  LENGTH: 120 amino acids
8  TYPE: amino acid
9  STRANDEDNESS: single
10  TOPOLOGY: linear
11  IMMEDIATE SOURCE:
12  LIBRARY: GenBank
13  JOURNAL: 1654516
14  SUBJECT: Descriptive; SEQ ID NO: 4:
15  US-09-822-295-4

16  Query Match: 28.0%; Score 45; DB 4; Length 120;
17  Best Local Similarity: 48.8%; Pred. No. 12;
18  Matches: 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

19  4 PYSKHQIIPNASVVKHSD 21
20  1 11 11 11 11 11
21  US-09-822-295-4
22  Sequence 3, Application US/08253785
23  Patent No. 6303372
24  GENERAL INFORMATION:
25  APPLICANT: Volpert, James L.
26  APPLICANT: Holt, Bruce M.
27  APPLICANT: Wurtolo, Eve S.
28  APPLICANT: Lupton, Paul S.
29  TITLE OF INVENTION: ROY PREFERENTIAL PROMOTER
30  NUMBER OF SEQUENCES: 1
31  CORRESPONDENT ADDRESS:
32  ADDRESS: Suido Aveo, Inc.,
33  STREET: 975 California Avenue
34  CITY: Palo Alto
35  STATE: CA
36  COUNTRY: USA
37  415-345-4
38  COMPUTER BEARER: IBM:
39  MEDIA TYPE: floppy disk
40  COMPUTER: IBM PC compatible
41  OPERATING SYSTEM: PC DOS/MS DOS
42  SOFTWARE: Patent to Release #1.0, Version #1.25
43  CURRENT APPLICATION DATA:
44  APPLICANT'S NUMBER: 05/08253785
45  FILING DATE:
46  CLASSIFICATION: 435
47  ACT BIRTH/ACCT INFORMATION:
48  NAME: Marcus Wenzel, Lynn
49  REPRESENTATIVE NUMBER: 14,869
50  REPRESENTATIVE NAME: 145-1089
51  TELEPHONE: 415/345-4588
52  TELEFAX: 415/345-4125
53  INFORMATION IN SEQ ID NO: 4:
54  SEQUENCE CHARACTERISTICS:
55  LENGTH: 600 amino acids
56  TYPE: amino acid
57  TOPOLOGY: linear
58  IMMEDIATE SOURCE:
59  LIBRARY: GenBank
60  JOURNAL: 1654516
61  SUBJECT: Descriptive; SEQ ID NO: 4:
62  US-09-822-295-4

63  Query Match: 28.0%; Score 45; DB 1; Length 600;
64  Best Local Similarity: 28.2%; Pred. No. 82;
65  Matches: 1; Conservative 0; Mismatches 8; Indels 14; Gaps 2;

66  4 PYSKHQIIPNASVVKHSD 29
67  1 11 11 11 11 11
68  US-09-822-295-4

```

```

69  Db: 428 SISVSHRSOBSI PTTSTPRTKSDYIMHMAVHHS 469

70  RESULT 13
71  US-09-208-742-2
72  Sequence 2, Application US/09208742
73  Patent No. 6174679
74  GENERAL INFORMATION:
75  APPLICANT: Kaufmann, Joerg
76  TITLE OF INVENTION: CTF150/HYAF1150 is Necessary for Cell
77  FILE REFERENCE: 1453,002
78  CURRENT APPLICATION NUMBER: us/09208742
79  CURRENT FILING DATE: 1998-12-10
80  NUMBER OF SEQ ID NOS: 6
81  SOFTWARE: FastSeq for Windows Version 3.0
82  SEQ ID NO: 2
83  LENGTH: 1199
84  TYPE: PRT
85  ORGANISM: human
86  US-09-208-742-2

87  Query Match: 28.0%; Score 45; DB 4; Length 1199;
88  Best Local Similarity: 34.8%; Pred. No. 196-02;
89  Matches: 5; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

90  4 PYSKHQIIPNASVVKHSD 26
91  1 11 11 11 11 11
92  US-09-342-295-4
93  Sequence 4, Application US/09342295
94  Patent No. 6303372
95  GENERAL INFORMATION:
96  APPLICANT: Kaufmann, Joerg
97  TITLE OF INVENTION: CTF130 INHIBITS CELL CYCLE PROGRESSION
98  FILE REFERENCE: 200130,456 / 1513,003
99  CURRENT APPLICATION NUMBER: us/09342295
100  CURRENT FILING DATE: 1999-06-11
101  NUMBER OF SEQ ID NOS: 4
102  SOFTWARE: FastSeq for Windows Version 3.0
103  SEQ ID NO: 4
104  LENGTH: 1199
105  TYPE: PRT
106  ORGANISM: Homo sapien
107  US-09-342-295-4

108  Query Match: 28.0%; Score 45; DB 4; Length 1199;
109  Best Local Similarity: 34.8%; Pred. No. 196-02;
110  Matches: 8; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

111  4 PYSKHQIIPNASVVKHSD 26
112  1 11 11 11 11 11
113  US-09-709-979-4
114  Sequence 4, Application US/09709979
115  Patent No. 6423822
116  GENERAL INFORMATION:
117  APPLICANT: Kaufmann, Joerg
118  TITLE OF INVENTION: CTF130 INHIBITS CELL CYCLE PROGRESSION
119  FILE REFERENCE: 200130,456 / 1513,003
120  CURRENT APPLICATION NUMBER: us/09709979
121  CURRENT FILING DATE: 2000-11-09
122  PRIOR APPLICATION NUMBER: US 99/152,295
123  PRIOR FILING DATE: 1999-06-11
124  NUMBER OF SEQ ID NOS: 4
125  SOFTWARE: FastSeq for Windows Version 3.0
126  SEQ ID NO: 4

```

1. [REDACTED]  
2. [REDACTED]  
3. [REDACTED]

4. [REDACTED]  
5. [REDACTED]  
6. [REDACTED]  
7. [REDACTED]  
8. [REDACTED]  
9. [REDACTED]  
10. [REDACTED]  
11. [REDACTED]  
12. [REDACTED]  
13. [REDACTED]  
14. [REDACTED]  
15. [REDACTED]  
16. [REDACTED]  
17. [REDACTED]  
18. [REDACTED]  
19. [REDACTED]  
20. [REDACTED]  
21. [REDACTED]  
22. [REDACTED]  
23. [REDACTED]  
24. [REDACTED]  
25. [REDACTED]  
26. [REDACTED]  
27. [REDACTED]  
28. [REDACTED]  
29. [REDACTED]  
30. [REDACTED]  
31. [REDACTED]  
32. [REDACTED]  
33. [REDACTED]  
34. [REDACTED]  
35. [REDACTED]  
36. [REDACTED]  
37. [REDACTED]  
38. [REDACTED]  
39. [REDACTED]  
40. [REDACTED]  
41. [REDACTED]  
42. [REDACTED]  
43. [REDACTED]  
44. [REDACTED]  
45. [REDACTED]  
46. [REDACTED]  
47. [REDACTED]  
48. [REDACTED]  
49. [REDACTED]  
50. [REDACTED]  
51. [REDACTED]  
52. [REDACTED]  
53. [REDACTED]  
54. [REDACTED]  
55. [REDACTED]  
56. [REDACTED]  
57. [REDACTED]  
58. [REDACTED]  
59. [REDACTED]  
60. [REDACTED]  
61. [REDACTED]  
62. [REDACTED]  
63. [REDACTED]  
64. [REDACTED]  
65. [REDACTED]  
66. [REDACTED]  
67. [REDACTED]  
68. [REDACTED]  
69. [REDACTED]  
70. [REDACTED]  
71. [REDACTED]  
72. [REDACTED]  
73. [REDACTED]  
74. [REDACTED]  
75. [REDACTED]  
76. [REDACTED]  
77. [REDACTED]  
78. [REDACTED]  
79. [REDACTED]  
80. [REDACTED]  
81. [REDACTED]  
82. [REDACTED]  
83. [REDACTED]  
84. [REDACTED]  
85. [REDACTED]  
86. [REDACTED]  
87. [REDACTED]  
88. [REDACTED]  
89. [REDACTED]  
90. [REDACTED]  
91. [REDACTED]  
92. [REDACTED]  
93. [REDACTED]  
94. [REDACTED]  
95. [REDACTED]  
96. [REDACTED]  
97. [REDACTED]  
98. [REDACTED]  
99. [REDACTED]  
100. [REDACTED]







```

1  MATCHES: 10; 29.2% Score 47; DB 9; Length 1115;
2  Best Local Similarity: 47.6%; Prot. No. 2.2e-022;
3  Matches: 10; Conservative: 2; Mismatches: 5; Gaps: 1;
4
5  1 YSLPYDKHQIRNSNVKHH 21
6  111
7  1002 YLAPDSIHQLDQ-- PHHD 1018
8
9  RESULT 11
10 US-10-175-752-440
11 Sequence 440, Application US/1176482
12 Publication No. US20040022296A1
13 GENERAL INFORMATION:
14 APPLICANT: Baker, Kevin P.
15 APPLICANT: Chen, Jiah
16 APPLICANT: Gadowski, Paul J.
17 APPLICANT: Gadowski, Paul J.
18 APPLICANT: Gadowski, Paul J.
19 APPLICANT: Gadowski, Paul J.
20 APPLICANT: Gadowski, Paul J.
21 APPLICANT: Gadowski, Paul J.
22 APPLICANT: Gadowski, Paul J.
23 APPLICANT: Gadowski, Paul J.
24 APPLICANT: Gadowski, Paul J.
25 APPLICANT: Gadowski, Paul J.
26 APPLICANT: Gadowski, Paul J.
27 APPLICANT: Gadowski, Paul J.
28 APPLICANT: Gadowski, Paul J.
29 APPLICANT: Gadowski, Paul J.
30 APPLICANT: Gadowski, Paul J.
31 APPLICANT: Gadowski, Paul J.
32 APPLICANT: Gadowski, Paul J.
33 APPLICANT: Gadowski, Paul J.
34 APPLICANT: Gadowski, Paul J.
35 APPLICANT: Gadowski, Paul J.
36 APPLICANT: Gadowski, Paul J.
37 APPLICANT: Gadowski, Paul J.
38 APPLICANT: Gadowski, Paul J.
39 APPLICANT: Gadowski, Paul J.
40 APPLICANT: Gadowski, Paul J.
41 APPLICANT: Gadowski, Paul J.
42 APPLICANT: Gadowski, Paul J.
43 APPLICANT: Gadowski, Paul J.
44 APPLICANT: Gadowski, Paul J.
45 APPLICANT: Gadowski, Paul J.
46 APPLICANT: Gadowski, Paul J.
47 APPLICANT: Gadowski, Paul J.
48 APPLICANT: Gadowski, Paul J.
49 APPLICANT: Gadowski, Paul J.
50 APPLICANT: Gadowski, Paul J.
51 APPLICANT: Gadowski, Paul J.
52 APPLICANT: Gadowski, Paul J.
53 APPLICANT: Gadowski, Paul J.
54 APPLICANT: Gadowski, Paul J.
55 APPLICANT: Gadowski, Paul J.
56 APPLICANT: Gadowski, Paul J.
57 APPLICANT: Gadowski, Paul J.
58 APPLICANT: Gadowski, Paul J.
59 APPLICANT: Gadowski, Paul J.
60 APPLICANT: Gadowski, Paul J.
61 APPLICANT: Gadowski, Paul J.
62 APPLICANT: Gadowski, Paul J.
63 APPLICANT: Gadowski, Paul J.
64 APPLICANT: Gadowski, Paul J.
65 APPLICANT: Gadowski, Paul J.
66 APPLICANT: Gadowski, Paul J.
67 APPLICANT: Gadowski, Paul J.
68 APPLICANT: Gadowski, Paul J.
69 APPLICANT: Gadowski, Paul J.
70 APPLICANT: Gadowski, Paul J.
71 APPLICANT: Gadowski, Paul J.
72 APPLICANT: Gadowski, Paul J.
73 APPLICANT: Gadowski, Paul J.
74 APPLICANT: Gadowski, Paul J.
75 APPLICANT: Gadowski, Paul J.
76 APPLICANT: Gadowski, Paul J.
77 APPLICANT: Gadowski, Paul J.
78 APPLICANT: Gadowski, Paul J.
79 APPLICANT: Gadowski, Paul J.
80 APPLICANT: Gadowski, Paul J.
81 APPLICANT: Gadowski, Paul J.
82 APPLICANT: Gadowski, Paul J.
83 APPLICANT: Gadowski, Paul J.
84 APPLICANT: Gadowski, Paul J.
85 APPLICANT: Gadowski, Paul J.
86 APPLICANT: Gadowski, Paul J.
87 APPLICANT: Gadowski, Paul J.
88 APPLICANT: Gadowski, Paul J.
89 APPLICANT: Gadowski, Paul J.
90 APPLICANT: Gadowski, Paul J.
91 APPLICANT: Gadowski, Paul J.
92 APPLICANT: Gadowski, Paul J.
93 APPLICANT: Gadowski, Paul J.
94 APPLICANT: Gadowski, Paul J.
95 APPLICANT: Gadowski, Paul J.
96 APPLICANT: Gadowski, Paul J.
97 APPLICANT: Gadowski, Paul J.
98 APPLICANT: Gadowski, Paul J.
99 APPLICANT: Gadowski, Paul J.
100 APPLICANT: Gadowski, Paul J.

```

```

1  APPLICANT: Watanabe, Colleen K.
2  APPLICANT: Wood, William L.
3  APPLICANT: Zhang, Zhenli
4  TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE POLYPEPTIDES AND NOVELLE
5  FILE REFERENCE: P44081945
6  CURRENT FILING DATE: 2002-06-19
7  PTO APPLICATION REMOVED: See File Wrapper or Palm
8  NUMBER OF SEQ ID NOS: 612
9  SEQ ID NO 440
10 LENGTH: 1115
11 TYPE: PRT
12 ORGANISM: Homo Sapien
13 US-10-175-738-440
14
15 Query Match: 29.2% Score 47; DB 9; Length 1115;
16 Best Local Similarity: 47.6%; Prot. No. 2.2e-022;
17 Matches: 10; Conservative: 2; Mismatches: 5; Gaps: 1;
18
19 1 YSLPYDKHQIRNSNVKHH 21
20 111
21 1002 YLAPDSIHQLDQ-- PHHD 1018
22
23 RESULT 12
24 US-10-176-482-440
25 Sequence 440, Application US/1176482
26 Publication No. US20040022296A1
27 GENERAL INFORMATION:
28 APPLICANT: Baker, Kevin P.
29 APPLICANT: Chen, Jiah
30 APPLICANT: Gadowski, Paul J.
31 APPLICANT: Gadowski, Paul J.
32 APPLICANT: Gadowski, Paul J.
33 APPLICANT: Gadowski, Paul J.
34 APPLICANT: Gadowski, Paul J.
35 APPLICANT: Gadowski, Paul J.
36 APPLICANT: Gadowski, Paul J.
37 APPLICANT: Gadowski, Paul J.
38 APPLICANT: Gadowski, Paul J.
39 APPLICANT: Gadowski, Paul J.
40 APPLICANT: Gadowski, Paul J.
41 APPLICANT: Gadowski, Paul J.
42 APPLICANT: Gadowski, Paul J.
43 APPLICANT: Gadowski, Paul J.
44 APPLICANT: Gadowski, Paul J.
45 APPLICANT: Gadowski, Paul J.
46 APPLICANT: Gadowski, Paul J.
47 APPLICANT: Gadowski, Paul J.
48 APPLICANT: Gadowski, Paul J.
49 APPLICANT: Gadowski, Paul J.
50 APPLICANT: Gadowski, Paul J.
51 APPLICANT: Gadowski, Paul J.
52 APPLICANT: Gadowski, Paul J.
53 APPLICANT: Gadowski, Paul J.
54 APPLICANT: Gadowski, Paul J.
55 APPLICANT: Gadowski, Paul J.
56 APPLICANT: Gadowski, Paul J.
57 APPLICANT: Gadowski, Paul J.
58 APPLICANT: Gadowski, Paul J.
59 APPLICANT: Gadowski, Paul J.
60 APPLICANT: Gadowski, Paul J.
61 APPLICANT: Gadowski, Paul J.
62 APPLICANT: Gadowski, Paul J.
63 APPLICANT: Gadowski, Paul J.
64 APPLICANT: Gadowski, Paul J.
65 APPLICANT: Gadowski, Paul J.
66 APPLICANT: Gadowski, Paul J.
67 APPLICANT: Gadowski, Paul J.
68 APPLICANT: Gadowski, Paul J.
69 APPLICANT: Gadowski, Paul J.
70 APPLICANT: Gadowski, Paul J.
71 APPLICANT: Gadowski, Paul J.
72 APPLICANT: Gadowski, Paul J.
73 APPLICANT: Gadowski, Paul J.
74 APPLICANT: Gadowski, Paul J.
75 APPLICANT: Gadowski, Paul J.
76 APPLICANT: Gadowski, Paul J.
77 APPLICANT: Gadowski, Paul J.
78 APPLICANT: Gadowski, Paul J.
79 APPLICANT: Gadowski, Paul J.
80 APPLICANT: Gadowski, Paul J.
81 APPLICANT: Gadowski, Paul J.
82 APPLICANT: Gadowski, Paul J.
83 APPLICANT: Gadowski, Paul J.
84 APPLICANT: Gadowski, Paul J.
85 APPLICANT: Gadowski, Paul J.
86 APPLICANT: Gadowski, Paul J.
87 APPLICANT: Gadowski, Paul J.
88 APPLICANT: Gadowski, Paul J.
89 APPLICANT: Gadowski, Paul J.
90 APPLICANT: Gadowski, Paul J.
91 APPLICANT: Gadowski, Paul J.
92 APPLICANT: Gadowski, Paul J.
93 APPLICANT: Gadowski, Paul J.
94 APPLICANT: Gadowski, Paul J.
95 APPLICANT: Gadowski, Paul J.
96 APPLICANT: Gadowski, Paul J.
97 APPLICANT: Gadowski, Paul J.
98 APPLICANT: Gadowski, Paul J.
99 APPLICANT: Gadowski, Paul J.
100 APPLICANT: Gadowski, Paul J.

```

```

1 APPLICANT: Gurney, Austin L.
2 APPLICANT: Pan, James
3 APPLICANT: Smith, Victoria L.
4 APPLICANT: Watanabe, Colin K.
5 APPLICANT: Wood, William L.
6 APPLICANT: Zhang, Zemin
7 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
8 FILE REFERENCE: P3430R1070
9 CURRENT FILING DATE: 2002-06-20
10 PRIOR APPLICATION REMOVED - See File Wrapper or Palm
11 SEQ ID NO: 440
12 LENGTH: 1115
13 TYPE: PRT
14 ORGANISM: Homo Sapien
15 US-10-176-913-440

```

```

Query Match          29.2% Score 47: DB 9: Length 1115
Best Local Similarity 47.6% Prod. No. 2,20+02:
Matches 10: Conservative 2: Mismatches 5: Indels 4: Gaps 1:

```

```

QY 1 YSLPYDSKHQIRNASVXKHHH 21
DE 1002 YTLPPDSTHQLQ----PHHD 1018

```

```

RESULT 15
US-10-176-757-440
Sequence 440: Application US/0176757
Publication No. US20030022297A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey J.
APPLICANT: Godzowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William L.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1070
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO: 440
LENGTH: 1115
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-757-440

```

```

Query Match          29.2% Score 47: DB 9: Length 1115
Best Local Similarity 47.6% Prod. No. 2,20+02:
Matches 10: Conservative 2: Mismatches 5: Indels 4: Gaps 1:

```

```

QY 1 YSLPYDSKHQIRNASVXKHHH 21
DE 1002 YTLPPDSTHQLQ----PHHD 1018

```

```

RESULT 14
US-10-176-913-440
Sequence 440: Application US/0176913
Publication No. US20030022298A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey J.
APPLICANT: Godzowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William L.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1070
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO: 440
LENGTH: 1115
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-913-440

```

```

1 APPLICANT: Desnoyers, Luc
2 APPLICANT: Goddard, Audrey
3 APPLICANT: Godzowski, Paul J.
4 APPLICANT: Gurney, Austin L.
5 APPLICANT: Pan, James
6 APPLICANT: Smith, Victoria L.
7 APPLICANT: Watanabe, Colin K.
8 APPLICANT: Wood, William L.
9 APPLICANT: Zhang, Zemin
10 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
11 FILE REFERENCE: P3430R1066
12 CURRENT APPLICATION NUMBER: 03/0176757, 914
13 CURRENT FILING DATE: 2002-06-20
14 PRIOR APPLICATION REMOVED - See File Wrapper or Palm
15 SEQ ID NO: 440
16 LENGTH: 1115
17 TYPE: PRT
18 ORGANISM: Homo Sapien
19 US-10-176-913-440

```

```

Query Match          29.2% Score 47: DB 9: Length 1115
Best Local Similarity 47.6% Prod. No. 2,20+02:
Matches 10: Conservative 2: Mismatches 5: Indels 4: Gaps 1:

```

```

QY 1 YSLPYDSKHQIRNASVXKHHH 21
DE 1002 YTLPPDSTHQLQ----PHHD 1018

```

```

RESULT 15
US-10-180-552-440
Sequence 440: Application US/10180552
Publication No. US20030022300A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godzowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William L.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1053
CURRENT APPLICATION NUMBER: 03/0180552
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO: 440
LENGTH: 1115
TYPE: PRT
ORGANISM: Homo Sapien
US-10-180-552-440

```

```

Query Match          29.2% Score 47: DB 9: Length 1115
Best Local Similarity 47.6% Prod. No. 2,20+02:
Matches 10: Conservative 2: Mismatches 5: Indels 4: Gaps 1:

```

```

QY 1 YSLPYDSKHQIRNASVXKHHH 21
DE 1002 YTLPPDSTHQLQ----PHHD 1018

```

```

Search completed: July 8, 2003, 12:27:34
Job time: 26.7033 secs

```

i  
u



ncbi version 3.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

MM Protein - Protein search, using SW model

Run on: July 8, 2003, 12:07:22 : Search time 11.8641 seconds  
(without alignments)

243,006 Million cell updates/sec

Protein Score: 154.1

Sequence: 1 YSLHYDSKHQITENASVKNHHSNAGVTSY 30

Standard Table: R03S0992

Input: 10.0 : Output: 0.5

Score: 28.124 seqs: 9614422 residues

Local Effect of hits satisfying chosen parameters: 28.124

Minimum DB seq length: 0

Maximum DB seq length: 2,000,000,000

Fast Processing: Minimum Match: 0.6

Maximum Match: 1.000

Lasting first 15 summaries

Database: 1 R03S0992  
2 R03S0992  
3 R03S0992  
4 R03S0992

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	56	459	2	137704
2	56	459	2	143538
3	52	459	2	143538
4	52	459	2	143538
5	52	459	2	143538
6	52	459	2	143538
7	52	459	2	143538
8	52	459	2	143538
9	52	459	2	143538
10	52	459	2	143538
11	52	459	2	143538
12	52	459	2	143538
13	52	459	2	143538
14	52	459	2	143538
15	52	459	2	143538
16	52	459	2	143538
17	52	459	2	143538
18	52	459	2	143538
19	52	459	2	143538
20	52	459	2	143538
21	52	459	2	143538
22	52	459	2	143538
23	52	459	2	143538
24	52	459	2	143538
25	52	459	2	143538
26	52	459	2	143538
27	52	459	2	143538
28	52	459	2	143538
29	52	459	2	143538
30	52	459	2	143538

## ALIGNMENTS

30	46	28.6	28.2	2	137704
31	46	28.6	44.1	2	143538
32	46	28.6	56.0	2	143538
33	46	28.6	66.2	2	143538
34	46	28.6	66.2	2	143538
35	46	28.6	66.2	2	143538
36	46	28.6	66.2	2	143538
37	46	28.6	66.2	2	143538
38	46	28.6	66.2	2	143538
39	46	28.6	66.2	2	143538
40	46	28.6	66.2	2	143538
41	46	28.6	66.2	2	143538
42	46	28.6	66.2	2	143538
43	46	28.6	66.2	2	143538
44	46	28.6	66.2	2	143538
45	46	28.6	66.2	2	143538

RESULT 1  
137704  
Zinc-finger protein ZPR1 - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #Sequence revision 03-Dec-1999 #Text update 21-Jun-2000  
C:Accession: T37704  
R:Murphy, L.; Harris, D.; Wood, V.; Petrolis, B.; Kojanovic, M.A.  
submitted to the EMBL Data Library, June 1997  
A:Reference number: 221738  
A:Accession: T37704  
A:Status: Preliminary; translated from cDNA; EST: T37704  
A:Molecule type: DNA  
A:Crosses: 1-459-2008  
A:Cross-References: EMBL:297099; PDB:1Q91; SRS:143538; SRS:143538; SRS:143538  
A:Experimental source: strain 972h7; cosmid c15A10  
C:Genetics:  
A:Gene: ZPR1; SPDB:SPAC15A10.04c  
A:Map position: 1  
C:Superfamily: hypothetical protein YGR211w

Query Match 34.88; Score 56; DB 2; Length 459;  
Best Local Similarity 50.0%; Prod. No. 2.47  
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
ID 224 PDSKHQITENASVKNHHSNAGVTSY 247  
RESULT 2  
143538  
Zinc-finger protein ZPR1 - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #Sequence revision 03-Dec-1999 #Text update 21-Jun-2000  
C:Accession: T43538  
R:Kojanovic, M.A.; Harris, D.; Wood, V.; Petrolis, B.; Kojanovic, M.A.  
submitted to the EMBL Data Library, August 1997  
A:Description: Translational regulation by the ZPR1 signal transduction pathway.  
A:Reference number: 222557  
A:Accession: T43538  
A:Status: Preliminary; translated from cDNA; EST: T43538  
A:Molecule type: DNA  
A:Crosses: 1-459-2008  
A:Cross-References: EMBL:297099; PDB:1Q91; SRS:143538; SRS:143538; SRS:143538  
C:Genetics:  
A:Gene: ZPR1  
C:Superfamily: hypothetical protein YGR211w  
Query Match 34.88; Score 56; DB 2; Length 459;  
Best Local Similarity 50.0%; Prod. No. 2.47  
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;







Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

Search time 6.58641 seconds  
(without alignment)

# ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS

ALIGNMENTS









RA Zsolt, Farkas M., Fritzel C., Holzer E., Moesl D., Hilbert H.,  
RA Borzym K., Jander L., Bress A., Behnisch B., Reinhardt R., Pohl T.M.,  
RA Ertl P., Zimmermann W., Wegler E., Wambolt K., Fauréteix R.,  
RA Gallez A., Cadet E., Lirio S., Gloux S., Lelaite V., Mottier S.,  
RA Gaillet P., Aves S.C., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Fries M., Nothel M., Gallardin G., Tallada V.A., Garçon A., Thode G.,  
RA Juras R.R., Ritzdorf J., Jhinetz J., Sánchez V., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J., Moreno S., Armstrong J., Forsburg S.L.,  
RA Vermeil P., Lowe T., McCombie W.R., Paulsen J., Potashkin J.,  
RA Shkumatkin G.V., Hesser B., Farrell B.G., Nurse P.,  
RA "The consense sequence of Schizosaccharomyces pombe";  
RA Nature 415:671-680(2002).  
RA FUNDATION FORS PRESENTIALLY, TO THE MAUNDRELL ARS CONSENSUS  
RA SEQUENCE WITHIN ARS002.  
RA SUBMITTALOR EMAILING: Nucleot.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (<http://www.ebi.ac.uk/ebd/seq/submit/>).

[illegible]

the Swiss Patent is copyleft. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by not-for-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement from [info@cas.org](mailto:info@cas.org).  
 CC or send an email to [license@cas.org](mailto:license@cas.org).  
 CC -----  
 DR EMBL: Z97178; CA090900.1; -  
 DR InterPro: IPR003640; ERF\_C  
 DR InterPro: IPR004161; ERFU\_D2  
 DR InterPro: IPR007955; EF-GTPbind.  
 DR Pfam: PF00009; GTP-EFTRP\_1.  
 DR Pfam: PF00679; ERF\_C\_1.  
 DR Pfam: PF03144; GTP-EFTU\_D2\_1  
 DR PROSITE: PS00301; EFACITOR\_GTP\_1.  
 KW Flocculation factor; GTP-binding; protein elongation factor; phosphorylation;  
 FT NP\_BIND 26 33 GTP (3Y SIMILARITY);  
 FT NP\_BIND 104 108 GTP (3Y SIMILARITY);  
 FT NP\_BIND 158 161 GTP (3Y SIMILARITY);  
 FT MOD\_RES 57 57 protein-lysine (3Y SIMILARITY);  
 FT MOD\_RES 59 59 phosphorylation (3Y SIMILARITY);  
 FT MOD\_RES 700 700 phosphatidyl (3Y SIMILARITY);  
 SS SEQUENCE 843 AA; 93799 MW; 0132584A1F4E8 (Method);

Query Match	23/26	score 47	EB 1	Length 843
Best Local Similarity	50.0%	Prag. No. 37		
Matches	11	Min Match	3	Indels

CC THE SWISS-PROT entry is copyright. It is produced through  
CC between the Swiss Institute of Bioinformatics and the EMBL  
CC the European Bioinformatics Institute. There are no restrictions  
CC use by non-profit institutions as long as its content is  
CC modified and this statement is not removed, altered or  
CC omitted; requests to license the content for other purposes  
CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk) or  
CC [EMBL@X99466; CAA67829.1; ...](mailto:EMBL@X99466; CAA67829.1; ...)  
DR InterPro: [www.ebi.ac.uk/InterPro](http://www.ebi.ac.uk/InterPro)  
DR Pfam: [Pfam](http://www.ebi.ac.uk/Pfam) PF02298; [Protein](http://www.ebi.ac.uk/Protein) Pfam  
DR Pfam: [Pfam](http://www.ebi.ac.uk/Pfam) PF06392; [Protein](http://www.ebi.ac.uk/Protein) Pfam  
DR Modulation: Signal.  
FT SIGNAL 1 22 HYDROPHILICITY  
FT CHAIN 23 180 EARLY MODULIN 16  
FT DOMAIN 24 180 EARLY-MODULIN-LIKE  
FT FT 2  
SQ SEQUENCE 180 AA; 20026 MW; 474742B75007066E CDS64;

1. **TO:** DIRECTOR, FBI  
 2. **FROM:** SAC, NEW YORK (100-100000)  
 3. **SUBJECT:** JAMES EARL RAY; AKA; ALIASES; FUGITIVE; MURDER OF MARTIN LUTHER KING, JR.; CIVIL RIGHTS; CONSPIRACY.  
 4. **RE:** NEW YORK TELETYPE TO BUREAU, APRIL TWENTY, LAST.  
 5. **REFERENCE:** BUREAU TELETYPE TO NEW YORK, APRIL TWENTY, LAST.  
 6. **DETAILS:** NEW YORK POLICE DEPARTMENT (NYPD) HAS ADVISED THAT IT HAS RECEIVED INFORMATION FROM AN INDIVIDUAL WHO OFFERS HIMSELF AS A WITNESS IN THE CASE OF THE ALLEGED CONSPIRACY TO ASSASSINATE MARTIN LUTHER KING, JR. THIS INDIVIDUAL, WHOSE NAME IS BEING KEPT CONFIDENTIAL AT THIS TIME, CLAIMS TO HAVE BEEN IN CONTACT WITH AN INDIVIDUAL WHO IS ALLEGED TO HAVE BEEN IN CONTACT WITH JAMES EARL RAY. THE INDIVIDUAL CLAIMS THAT HE HAS BEEN OFFERED A LARGE SUM OF MONEY TO ASSIST IN THE ATTEMPTED ASSASSINATION OF KING. THE INDIVIDUAL CLAIMS THAT HE HAS REFUSED THE OFFER AND WANTS TO REPORT THE MATTER TO THE FBI. THE INDIVIDUAL CLAIMS THAT HE HAS BEEN OFFERED A LARGE SUM OF MONEY TO ASSIST IN THE ATTEMPTED ASSASSINATION OF KING. THE INDIVIDUAL CLAIMS THAT HE HAS REFUSED THE OFFER AND WANTS TO REPORT THE MATTER TO THE FBI. THE INDIVIDUAL CLAIMS THAT HE HAS BEEN OFFERED A LARGE SUM OF MONEY TO ASSIST IN THE ATTEMPTED ASSASSINATION OF KING. THE INDIVIDUAL CLAIMS THAT HE HAS REFUSED THE OFFER AND WANTS TO REPORT THE MATTER TO THE FBI.

01 (protoc) A)  
 02 At Atlantic halibut nervous necrosis virus (AANNV).  
 03 Virus: ssRNA, positive strand virus, no DNA stage. Nucleotide  
 04 nucleotide is:  
 05 NCHL10111-19489:  
 06  
 07  
 08  
 09  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517





Open version 6.1.6  
Copyright (c) 1994-2003 CompuGen Ltd

• **Model for cell proliferation**, using SW model

Year	Search time (seconds)	Updates/second
2004	23.7663	260.421
2005	23.7663	260.421
2006	23.7663	260.421
2007	23.7663	260.421
2008	23.7663	260.421
2009	23.7663	260.421
2010	23.7663	260.421
2011	23.7663	260.421
2012	23.7663	260.421
2013	23.7663	260.421
2014	23.7663	260.421
2015	23.7663	260.421
2016	23.7663	260.421
2017	23.7663	260.421
2018	23.7663	260.421
2019	23.7663	260.421
2020	23.7663	260.421
2021	23.7663	260.421
2022	23.7663	260.421
2023	23.7663	260.421
2024	23.7663	260.421
2025	23.7663	260.421
2026	23.7663	260.421
2027	23.7663	260.421
2028	23.7663	260.421
2029	23.7663	260.421
2030	23.7663	260.421

— YLEIPIKSIKÄNÄSVÄHÖSSÄICVSY 30

# Appendix C

2004047115 residues

For all values of  $\alpha$ , the chosen parameters are: 67, 530

[illegible]

1.  $f_1$   
 2.  $f_2$   
 3.  $f_3$   
 4.  $f_4$   
 5.  $f_5$   
 6.  $f_6$   
 7.  $f_7$   
 8.  $f_8$   
 9.  $f_9$   
 10.  $f_{10}$   
 11.  $f_{11}$   
 12.  $f_{12}$   
 13.  $f_{13}$   
 14.  $f_{14}$   
 15.  $f_{15}$   
 16.  $f_{16}$   
 17.  $f_{17}$   
 18.  $f_{18}$   
 19.  $f_{19}$   
 20.  $f_{20}$   
 21.  $f_{21}$   
 22.  $f_{22}$   
 23.  $f_{23}$   
 24.  $f_{24}$   
 25.  $f_{25}$   
 26.  $f_{26}$   
 27.  $f_{27}$   
 28.  $f_{28}$   
 29.  $f_{29}$   
 30.  $f_{30}$   
 31.  $f_{31}$   
 32.  $f_{32}$   
 33.  $f_{33}$   
 34.  $f_{34}$   
 35.  $f_{35}$   
 36.  $f_{36}$   
 37.  $f_{37}$   
 38.  $f_{38}$   
 39.  $f_{39}$   
 40.  $f_{40}$   
 41.  $f_{41}$   
 42.  $f_{42}$   
 43.  $f_{43}$   
 44.  $f_{44}$   
 45.  $f_{45}$   
 46.  $f_{46}$   
 47.  $f_{47}$   
 48.  $f_{48}$   
 49.  $f_{49}$   
 50.  $f_{50}$   
 51.  $f_{51}$   
 52.  $f_{52}$   
 53.  $f_{53}$   
 54.  $f_{54}$   
 55.  $f_{55}$   
 56.  $f_{56}$   
 57.  $f_{57}$   
 58.  $f_{58}$   
 59.  $f_{59}$   
 60.  $f_{60}$   
 61.  $f_{61}$   
 62.  $f_{62}$   
 63.  $f_{63}$   
 64.  $f_{64}$   
 65.  $f_{65}$   
 66.  $f_{66}$   
 67.  $f_{67}$   
 68.  $f_{68}$   
 69.  $f_{69}$   
 70.  $f_{70}$   
 71.  $f_{71}$   
 72.  $f_{72}$   
 73.  $f_{73}$   
 74.  $f_{74}$   
 75.  $f_{75}$   
 76.  $f_{76}$   
 77.  $f_{77}$   
 78.  $f_{78}$   
 79.  $f_{79}$   
 80.  $f_{80}$   
 81.  $f_{81}$   
 82.  $f_{82}$   
 83.  $f_{83}$   
 84.  $f_{84}$   
 85.  $f_{85}$   
 86.  $f_{86}$   
 87.  $f_{87}$   
 88.  $f_{88}$   
 89.  $f_{89}$   
 90.  $f_{90}$   
 91.  $f_{91}$   
 92.  $f_{92}$   
 93.  $f_{93}$   
 94.  $f_{94}$   
 95.  $f_{95}$   
 96.  $f_{96}$   
 97.  $f_{97}$   
 98.  $f_{98}$   
 99.  $f_{99}$   
 100.  $f_{100}$

Maximum Moisture	Maximum Moisture
100%	100%

$\frac{d}{dx}$

$\frac{d^2}{dx^2}$

$\frac{d^3}{dx^3}$

$\frac{d^4}{dx^4}$

$\frac{d^5}{dx^5}$

$\frac{d^6}{dx^6}$

$\frac{d^7}{dx^7}$

$\frac{d^8}{dx^8}$

$\frac{d^9}{dx^9}$

$\frac{d^{10}}{dx^{10}}$

$\frac{d^{11}}{dx^{11}}$

$\frac{d^{12}}{dx^{12}}$

$\frac{d^{13}}{dx^{13}}$

$\frac{d^{14}}{dx^{14}}$

$\frac{d^{15}}{dx^{15}}$

$\frac{d^{16}}{dx^{16}}$

$\frac{d^{17}}{dx^{17}}$

$\frac{d^{18}}{dx^{18}}$

$\frac{d^{19}}{dx^{19}}$

$\frac{d^{20}}{dx^{20}}$

$\frac{d^{21}}{dx^{21}}$

$\frac{d^{22}}{dx^{22}}$

$\frac{d^{23}}{dx^{23}}$

$\frac{d^{24}}{dx^{24}}$

$\frac{d^{25}}{dx^{25}}$

$\frac{d^{26}}{dx^{26}}$

$\frac{d^{27}}{dx^{27}}$

$\frac{d^{28}}{dx^{28}}$

$\frac{d^{29}}{dx^{29}}$

$\frac{d^{30}}{dx^{30}}$

$\frac{d^{31}}{dx^{31}}$

$\frac{d^{32}}{dx^{32}}$

$\frac{d^{33}}{dx^{33}}$

$\frac{d^{34}}{dx^{34}}$

$\frac{d^{35}}{dx^{35}}$

$\frac{d^{36}}{dx^{36}}$

$\frac{d^{37}}{dx^{37}}$

$\frac{d^{38}}{dx^{38}}$

$\frac{d^{39}}{dx^{39}}$

$\frac{d^{40}}{dx^{40}}$

$\frac{d^{41}}{dx^{41}}$

$\frac{d^{42}}{dx^{42}}$

$\frac{d^{43}}{dx^{43}}$

$\frac{d^{44}}{dx^{44}}$

$\frac{d^{45}}{dx^{45}}$

$\frac{d^{46}}{dx^{46}}$

$\frac{d^{47}}{dx^{47}}$

$\frac{d^{48}}{dx^{48}}$

$\frac{d^{49}}{dx^{49}}$

$\frac{d^{50}}{dx^{50}}$

$\frac{d^{51}}{dx^{51}}$

$\frac{d^{52}}{dx^{52}}$

$\frac{d^{53}}{dx^{53}}$

$\frac{d^{54}}{dx^{54}}$

$\frac{d^{55}}{dx^{55}}$

$\frac{d^{56}}{dx^{56}}$

$\frac{d^{57}}{dx^{57}}$

$\frac{d^{58}}{dx^{58}}$

$\frac{d^{59}}{dx^{59}}$

$\frac{d^{60}}{dx^{60}}$

$\frac{d^{61}}{dx^{61}}$

$\frac{d^{62}}{dx^{62}}$

$\frac{d^{63}}{dx^{63}}$

$\frac{d^{64}}{dx^{64}}$

$\frac{d^{65}}{dx^{65}}$

$\frac{d^{66}}{dx^{66}}$

$\frac{d^{67}}{dx^{67}}$

$\frac{d^{68}}{dx^{68}}$

$\frac{d^{69}}{dx^{69}}$

$\frac{d^{70}}{dx^{70}}$

$\frac{d^{71}}{dx^{71}}$

$\frac{d^{72}}{dx^{72}}$

$\frac{d^{73}}{dx^{73}}$

$\frac{d^{74}}{dx^{74}}$

$\frac{d^{75}}{dx^{75}}$

$\frac{d^{76}}{dx^{76}}$

$\frac{d^{77}}{dx^{77}}$

$\frac{d^{78}}{dx^{78}}$

$\frac{d^{79}}{dx^{79}}$

$\frac{d^{80}}{dx^{80}}$

$\frac{d^{81}}{dx^{81}}$

$\frac{d^{82}}{dx^{82}}$

$\frac{d^{83}}{dx^{83}}$

$\frac{d^{84}}{dx^{84}}$

$\frac{d^{85}}{dx^{85}}$

$\frac{d^{86}}{dx^{86}}$

$\frac{d^{87}}{dx^{87}}$

$\frac{d^{88}}{dx^{88}}$

$\frac{d^{89}}{dx^{89}}$

$\frac{d^{90}}{dx^{90}}$

$\frac{d^{91}}{dx^{91}}$

$\frac{d^{92}}{dx^{92}}$

$\frac{d^{93}}{dx^{93}}$

$\frac{d^{94}}{dx^{94}}$

$\frac{d^{95}}{dx^{95}}$

$\frac{d^{96}}{dx^{96}}$

$\frac{d^{97}}{dx^{97}}$

$\frac{d^{98}}{dx^{98}}$

$\frac{d^{99}}{dx^{99}}$

$\frac{d^{100}}{dx^{100}}$

$\frac{d^{101}}{dx^{101}}$

$\frac{d^{102}}{dx^{102}}$

$\frac{d^{103}}{dx^{103}}$

$\frac{d^{104}}{dx^{104}}$

$\frac{d^{105}}{dx^{105}}$

$\frac{d^{106}}{dx^{106}}$

$\frac{d^{107}}{dx^{107}}$

$\frac{d^{108}}{dx^{108}}$

$\frac{d^{109}}{dx^{109}}$

$\frac{d^{110}}{dx^{110}}$

$\frac{d^{111}}{dx^{111}}$

$\frac{d^{112}}{dx^{112}}$

$\frac{d^{113}}{dx^{113}}$

$\frac{d^{114}}{dx^{114}}$

$\frac{d^{115}}{dx^{115}}$

$\frac{d^{116}}{dx^{116}}$

$\frac{d^{117}}{dx^{117}}$

$\frac{d^{118}}{dx^{118}}$

$\frac{d^{119}}{dx^{119}}$

$\frac{d^{120}}{dx^{120}}$

$\frac{d^{121}}{dx^{121}}$

$\frac{d^{122}}{dx^{122}}$

$\frac{d^{123}}{dx^{123}}$

$\frac{d^{124}}{dx^{124}}$

$\frac{d^{125}}{dx^{125}}$

$\frac{d^{126}}{dx^{126}}$

$\frac{d^{127}}{dx^{127}}$

$\frac{d^{128}}{dx^{128}}$

$\frac{d^{129}}{dx^{129}}$

$\frac{d^{130}}{dx^{130}}$

$\frac{d^{131}}{dx^{131}}$

$\frac{d^{132}}{dx^{132}}$

$\frac{d^{133}}{dx^{133}}$

$\frac{d^{134}}{dx^{134}}$

$\frac{d^{135}}{dx^{135}}$

$\frac{d^{136}}{dx^{136}}$

$\frac{d^{137}}{dx^{137}}$

$\frac{d^{138}}{dx^{138}}$

$\frac{d^{139}}{dx^{139}}$

$\frac{d^{140}}{dx^{140}}$

$\frac{d^{141}}{dx^{141}}$

$\frac{d^{142}}{dx^{142}}$

$\frac{d^{143}}{dx^{143}}$

$\frac{d^{144}}{dx^{144}}$

$\frac{d^{145}}{dx^{145}}$

$\frac{d^{146}}{dx^{146}}$

$\frac{d^{147}}{dx^{147}}$

$\frac{d^{148}}{dx^{148}}$

$\frac{d^{149}}{dx^{149}}$

$\frac{d^{150}}{dx^{150}}$

$\frac{d^{151}}{dx^{151}}$

$\frac{d^{152}}{dx^{152}}$

$\frac{d^{153}}{dx^{153}}$

$\frac{d^{154}}{dx^{154}}$

$\frac{d^{155}}{dx^{155}}$

$\frac{d^{156}}{dx^{156}}$

$\frac{d^{157}}{dx^{157}}$

$\frac{d^{158}}{dx^{158}}$

$\frac{d^{159}}{dx^{159}}$

$\frac{d^{160}}{dx^{160}}$

$\frac{d^{161}}{dx^{161}}$

$\frac{d^{162}}{dx^{162}}$

$\frac{d^{163}}{dx^{163}}$

$\frac{d^{164}}{dx^{164}}$

$\frac{d^{165}}{dx^{165}}$

$\frac{d^{166}}{dx^{166}}$

$\frac{d^{167}}{dx^{167}}$

$\frac{d^{168}}{dx^{168}}$

$\frac{d^{169}}{dx^{169}}$

$\frac{d^{170}}{dx^{170}}$

$\frac{d^{171}}{dx^{171}}$

$\frac{d^{172}}{dx^{172}}$

$\frac{d^{173}}{dx^{173}}$

$\frac{d^{174}}{dx^{174}}$

$\frac{d^{175}}{dx^{175}}$

$\frac{d^{176}}{dx^{176}}$

$\frac{d^{177}}{dx^{177}}$

$\frac{d^{178}}{dx^{178}}$

$\frac{d^{179}}{dx^{179}}$

$\frac{d^{180}}{dx^{180}}$

$\frac{d^{181}}{dx^{181}}$

$\frac{d^{182}}{dx^{182}}$

$\frac{d^{183}}{dx^{183}}$

$\frac{d^{184}}{dx^{184}}$

$\frac{d^{185}}{dx^{185}}$

$\frac{d^{186}}{dx^{186}}$

$\frac{d^{187}}{dx^{187}}$

$\frac{d^{188}}{dx^{188}}$

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

[illegible]

Notes: Numbers in the margin of results predicted by chance. I have a  $\chi^2$  test to measure that is equal to the score of the result being printed and is derived by analyzing all the total score distribution.

## SUMMARY

Pos. 1 (bp)	ID	Contig B	Match	Score	NCBI
990102	Q99012	4	100	100	Q99012
990105	Q99015	11	100	100	Q99015
990111	Q99011	11	100	100	Q99011
990116	Q99016	11	100	100	Q99016
990134	Q99034	11	100	100	Q99034
990141	Q99041	11	100	100	Q99041
990179	Q99079	11	100	100	Q99079
990182	Q99182	10	100	100	Q99182
990186	Q99086	12	100	100	Q99086
990191	Q99191	12	100	100	Q99191
990198	Q99198	18	100	100	Q99198
990201	Q99201	18	100	100	Q99201
990204	Q99204	18	100	100	Q99204
990211	Q99211	14	100	100	Q99211
990216	Q99216	16	100	100	Q99216
990218	Q99218	16	100	100	Q99218
990226	Q99226	16	100	100	Q99226
990234	Q99234	16	100	100	Q99234

17	50	41.1	614	10	Q96Y53	Q96Y53
18	50	41.1	689	6	Q96Y53	Q96Y53
19	49	40.4	194	10	Q43431	Q43431
20	49	40.4	468	8	Q78032	Q78032
21	49	40.4	520	16	Q96Y50	Q96Y50
22	49	40.4	1092	8	Q96Y57	Q96Y57
23	49	40.4	1692	8	Q96Y55	Q96Y55
24	49	40.4	1250	8	Q94395	Q94395
25	49	40.4	1292	8	Q90336	Q90336
26	45	40.1	2495	9	Q96Y44	Q96Y44
27	48.5	40.1	212	16	Q96Y43	Q96Y43
28	48.5	40.1	424	18	Q96Y45	Q96Y45
29	48.5	40.1	918	12	Q90266	Q90266
30	48.5	40.1	597	12	Q96Y46	Q96Y46
31	48.5	40.1	1423	10	Q96Y47	Q96Y47
32	48	29.8	423	10	Q96Y49	Q96Y49
33	48	29.8	433	10	Q96Y47	Q96Y47
34	48	29.8	447	10	Q96Y51	Q96Y51
35	48	29.8	451	10	Q96Y59	Q96Y59
36	48	29.8	459	10	Q96Y53	Q96Y53
37	48	29.8	554	10	Q96Y51	Q96Y51
38	47.5	29.5	365	16	Q96Y50	Q96Y50
39	47.5	29.5	737	12	Q96Y50	Q96Y50
40	47.5	29.5	3610	5	Q96Y47	Q96Y47
41	47.5	29.5	3620	5	Q96Y46	Q96Y46
42	47.5	29.5	3628	5	Q96Y47	Q96Y47
43	47.5	29.5	193	10	Q96Y47	Q96Y47
44	47	29.2	481	17	Q96Y43	Q96Y43
45	47	29.2				

## ALTERNATIVES

[illegible]

















1 66141 DENNIE  
 2 INFORMATION FOR SEQ ID NO: 1:  
 3 SEQUENCE CHARACTERISTICS:  
 4 LENGTH: 443 amino acids  
 5 TYPE: amino acid  
 6 TOPOLOGY: linear  
 7 MULTIPLE TYPE: protein  
 8 HYPOTHEICAL: NO  
 9 ANTI-SENSE: NO  
 10 ORIGINAL SOURCE:  
 11 ORGANISM: Acetobacter xylium  
 12 SEQ ID NO: 1  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500

1 66141 DENNIE  
 2 INFORMATION FOR SEQ ID NO: 1:  
 3 SEQUENCE CHARACTERISTICS:  
 4 LENGTH: 443 amino acids  
 5 TYPE: amino acid  
 6 TOPOLOGY: linear  
 7 MULTIPLE TYPE: protein  
 8 HYPOTHEICAL: NO  
 9 ANTI-SENSE: NO  
 10 ORIGINAL SOURCE:  
 11 ORGANISM: Acetobacter xylium  
 12 SEQ ID NO: 1  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500



RESULT 14  
 US-08-477-108A-2  
 Sequence 2, Application US/08/21714  
 Parent No. 5801001  
 GENERAL INFORMATION:  
 APPLICANT: Sadger, Ruth  
 APPLICANT: Zou, Zhigang  
 TITLE OF INVENTION: MASPIN, A NOVEL SERP N WITH  
 TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" floppy, 1.44 MB  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/21714  
 FILING DATE: 09/01/92  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/038,823  
 FILING DATE: 09/01/92  
 APPLICATION NUMBER: 07/844,296  
 FILING DATE: 02/28/92  
 APPLICATION NUMBER: 07/662,216  
 FILING DATE: 02/28/91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Judith K.  
 PRACTICE/PHONE NUMBER: 34, 919  
 TELEPHONE/DOCKING NUMBER: 006/07072001  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 375  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-121-714-2  
 Query Match: 29.7% Score 47; DB 4; Length 832;  
 Best Local Similarity: 41.7%; Prol. No. 28;  
 Matches: 10; Conservative: 5; Mismatches: 9; Indels: 0; Gaps: 0;

RESULT 14  
 US-08-477-108A-2  
 Sequence 2, Application US/08/21714  
 Parent No. 5801001  
 GENERAL INFORMATION:  
 APPLICANT: Sadger, Ruth  
 APPLICANT: Zou, Zhigang  
 TITLE OF INVENTION: MASPIN, A NOVEL SERP N WITH  
 TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" floppy, 1.44 MB  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/21714  
 FILING DATE: 09/01/92  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/121,714  
 FILING DATE: 09/01/93  
 APPLICATION NUMBER: 07/948,823  
 FILING DATE: 09/01/92





Database version 5.1.6  
 (c) 1994 - 2003 Compuser Inc.

Database search, used sw model

July 8, 2003 12:04:11 Search time 29.4407 seconds  
 (without alignments)

106,245 Million cell updates/sec

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Database version 5.1.6

Sequence: LACADSYSPNFKSTKAKMMNQVTRG 30

Table N: The number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

N	Score	Match	Count	Prob	Description
1	108	100%	60	2	AAV9259
2	107	100%	42	2	AAV28653
3	106	100%	30	2	AAV28653
4	105	100%	22	2	AAV28653
5	104	100%	16	2	AAV28653
6	103	100%	12	2	AAV28653
7	102	100%	9	2	AAV28653
8	101	100%	7	2	AAV28653
9	100	100%	5	2	AAV28653
10	99	100%	4	2	AAV28653
11	98	100%	3	2	AAV28653
12	97	100%	2	2	AAV28653
13	96	100%	2	2	AAV28653
14	95	100%	2	2	AAV28653
15	94	100%	2	2	AAV28653
16	93	100%	2	2	AAV28653
17	92	100%	2	2	AAV28653
18	91	100%	2	2	AAV28653
19	90	100%	2	2	AAV28653
20	89	100%	2	2	AAV28653
21	88	100%	2	2	AAV28653
22	87	100%	2	2	AAV28653
23	86	100%	2	2	AAV28653
24	85	100%	2	2	AAV28653
25	84	100%	2	2	AAV28653
26	83	100%	2	2	AAV28653
27	82	100%	2	2	AAV28653
28	81	100%	2	2	AAV28653
29	80	100%	2	2	AAV28653
30	79	100%	2	2	AAV28653

11	52	32.9	341	21	AAV28653	Human tyrosine phosphatase
12	51.5	32.6	347	22	AAV28653	Human tyrosine phosphatase
13	50	31.6	402	23	AAV28653	Human tyrosine phosphatase
14	48	30.4	421	21	AAV28653	Human tyrosine phosphatase
15	48	30.4	421	22	AAV28653	Human tyrosine phosphatase
16	48	30.4	421	22	AAV28653	Human tyrosine phosphatase
17	48	30.4	421	22	AAV28653	Human tyrosine phosphatase
18	48	30.4	421	22	AAV28653	Human tyrosine phosphatase
19	48	30.4	421	22	AAV28653	Human tyrosine phosphatase
20	48	30.4	421	22	AAV28653	Human tyrosine phosphatase
21	48	30.4	421	22	AAV28653	Human tyrosine phosphatase
22	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
23	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
24	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
25	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
26	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
27	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
28	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
29	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
30	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
31	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
32	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
33	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
34	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
35	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
36	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
37	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
38	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
39	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
40	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
41	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
42	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
43	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
44	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
45	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
46	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
47	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
48	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
49	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
50	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
51	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
52	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
53	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
54	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
55	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
56	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
57	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
58	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
59	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
60	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
61	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
62	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
63	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
64	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
65	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
66	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
67	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
68	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
69	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
70	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
71	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
72	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
73	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
74	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
75	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
76	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
77	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
78	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
79	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
80	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
81	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
82	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
83	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
84	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
85	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
86	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
87	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
88	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
89	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
90	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
91	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
92	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
93	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
94	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
95	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
96	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
97	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
98	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
99	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase
100	47.5	30.1	282	23	AAV28653	Human tyrosine phosphatase









[illegible]

AAAF59698	
10	AAF2203E standard protein, 1st AA.
XX	
A:	AAF50808;
XX	
01	27-MAR-2001 (first entry)
XX	
1d	Breast and ovarian cancer associated antigen protein sequence Sfig II 606.
XX	
KM	Human; breast cancer; ovarian cancer; cysticallity; immunosuppressive;
KM	neutrophic; neutrophilic; antiviral; antileukemic; hepatotropic;
KM	antibacterial; antiparasitic; antitumor; cytotoxic; antifungal;
KW	Addison's disease; allergy; autoimmune hemolytic anemia;
KW	multiple sclerosis; rheumatoid arthritis; chronic disease;
KM	cardiovascular disorder; wound healing; neurological disease;
XX	
0S	Homo sapiens;
XX	
FN	W02009F517-A1.
XX	
1D	21-SEP-2000.
XX	
FF	09 MAR 2000; 2000WO 0505881.
XX	
FX	12-MAR-1990; 900US 0124270.
XX	
1A	(HRA ) IPYMAN :RHWB:CTI :IN).
XX	
F1	Rosen CA, Ruben SM
LK	WPt: 2000 611615/58.
LK	N-PDB: AAF21m07.
XX	
1P	New human breast and ovarian cancer associated gene sequences and the
1P	polypeptides encoded by these genes, useful in the prevention,
1P	treatment and diagnosis of cancer, immune disorders, cardiovascular
PX	disorders and neurological diseases .
XX	
TS	Claim 11: Page 1045-1047; 1299pp; English.
XX	
CC	Sequences AAF21614 - AAF22041 represent DNA sequences encoding human
CC	proteins AAB0721 - AAB09128. The DNA and protein sequences are
CC	associated with breast and ovarian cancer. Included in the invention are
CC	sequences AAF22032 - AAF22040 and AAF09229 which are used in the
CC	isolation and characterization of the DNA and protein sequences of the
CC	invention. The breast and ovarian cancer associated DNA, proteins, agonist
CC	or antagonist sequences exhibit cytotoxic, immunosuppressive,
CC	neoplastic neuroprotective, antiviral, antileukemic, hepatotropic,
CC	antidiabetic, antiinflammatory, antitumor, cytotoxic, anticonvulsant,
CC	antibacterial, antitubercular and parasitic and cardiac activity. The
CC	polymerized and protein sequences are used in the diagnosis of cancer,
CC	particularly breast and ovarian cancer. The nucleic acid sequences,
CC	proteins, agonists and antagonists may also be used in the diagnosis,
CC	prevention and treatment of immune disorders e.g. Addison's disease,
CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC	arthritis and directed live cellitis, cardiovascular disorders such as
CC	myocardial ischemia; wound healing; neurological diseases such as
CC	peripheral neuropathy and epilepsy; and infectious diseases.
XX	
XX	Sequence 341 AA:
Query Match	42.9% Score 52 Pk 21 Length 341
best local Similarity	47.4% Prod. Nr. 7.22
Matches	92 Conservative 62 Mismatches 52 Indels 02 Gaps 02
4 CAGCGTGGGTCCTCAAA 22	
T T T T T T T T T T	
154 TAGGTGTTATKSHSAKV 172	
00	

















	1999	2000
Page 10	10	10
Page 11	11	11
Page 12	12	12
Page 13	13	13
Page 14	14	14
Page 15	15	15
Page 16	16	16
Page 17	17	17
Page 18	18	18
Page 19	19	19
Page 20	20	20
Page 21	21	21
Page 22	22	22
Page 23	23	23
Page 24	24	24
Page 25	25	25
Page 26	26	26
Page 27	27	27
Page 28	28	28
Page 29	29	29
Page 30	30	30
Page 31	31	31
Page 32	32	32
Page 33	33	33
Page 34	34	34
Page 35	35	35
Page 36	36	36
Page 37	37	37
Page 38	38	38
Page 39	39	39
Page 40	40	40
Page 41	41	41
Page 42	42	42
Page 43	43	43
Page 44	44	44
Page 45	45	45
Page 46	46	46
Page 47	47	47
Page 48	48	48
Page 49	49	49
Page 50	50	50
Page 51	51	51
Page 52	52	52
Page 53	53	53
Page 54	54	54
Page 55	55	55
Page 56	56	56
Page 57	57	57
Page 58	58	58
Page 59	59	59
Page 60	60	60
Page 61	61	61
Page 62	62	62
Page 63	63	63
Page 64	64	64
Page 65	65	65
Page 66	66	66
Page 67	67	67
Page 68	68	68
Page 69	69	69
Page 70	70	70
Page 71	71	71
Page 72	72	72
Page 73	73	73
Page 74	74	74
Page 75	75	75
Page 76	76	76
Page 77	77	77
Page 78	78	78
Page 79	79	79
Page 80	80	80
Page 81	81	81
Page 82	82	82
Page 83	83	83
Page 84	84	84
Page 85	85	85
Page 86	86	86
Page 87	87	87
Page 88	88	88
Page 89	89	89
Page 90	90	90
Page 91	91	91
Page 92	92	92
Page 93	93	93
Page 94	94	94
Page 95	95	95
Page 96	96	96
Page 97	97	97
Page 98	98	98
Page 99	99	99
Page 100	100	100

© 2000 Blackwell Science Ltd  
Journal of Internal Medicine 247: 369–376

THE UNIVERSITY OF CHICAGO

1. The first group of authors (e.g., [1, 2]) has shown that the use of the  $\epsilon$ - $\delta$  definition of the limit is not convenient for the study of the properties of the limit of a function. The second group of authors (e.g., [3, 4]) has shown that the use of the  $\epsilon$ - $\delta$  definition of the limit is not convenient for the study of the properties of the limit of a function.

need to see the benefit of people's protected by electronic information that is equal to the score of the result in the test. The need to protect the score of the score of the result in the test.

$\alpha$	$\beta$	$\gamma$	$\delta$	$\epsilon$	$\zeta$	$\eta$	$\theta$	$\iota$	$\kappa$	$\lambda$	$\mu$	$\nu$	$\xi$	$\omicron$	$\pi$	$\rho$	$\sigma$	$\tau$	$\upsilon$	$\phi$	$\chi$	$\psi$	$\omega$
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

## ACKNOWLEDGMENTS

RECEIVED  
JAN 19 1962

Journal of Applied Social Psychology, 30(1998)22-29

ALICE: I'm not a cat.

# MINERALS OF THE

APPROXIMATE  
STRENGTH

City: Los Angeles

SPATIAL: CAL  
COUNTY: 4

21P: 900071  
COMPUTER KENALDAI

# Math 101

COMPULSIVE  
OPERATIONAL  
CONFIDENCE

CURRENT AFFAIRS

CLASSIFIED

# THE UNIVERSITY OF CHICAGO

NAME: WILL  
KHOISIKAI

PLATE 10

TELEPHONE:  
TELEFAX: 0

THESE: 47  
UNIVERSITY OF KENT

SEQUENCE: CHAKA  
END: 51



1 PRIOR APPLICATION NUMBER: 1998-08-24  
 2 PRIOR FILING DATE: 1997-08-27  
 3 PRIOR FILING DATE: 1997-08-27  
 4 SOFTWARE: PATOUT VORSTION 4.0  
 5 SEQ ID NO: 0  
 6 LENGTH: 2442  
 7 TYPE: PRT  
 8 ORGANISM: human  
 9 US: 10 109 886 10

11 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 12 111 2442 36.48 Pred. No. 3.86+022  
 13 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

14 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 15 111 2442 36.48 Pred. No. 3.86+022  
 16 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

17 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 18 111 2442 36.48 Pred. No. 3.86+022  
 19 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

20 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 21 111 2442 36.48 Pred. No. 3.86+022  
 22 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

23 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 24 111 2442 36.48 Pred. No. 3.86+022  
 25 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

26 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 27 111 2442 36.48 Pred. No. 3.86+022  
 28 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

29 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 30 111 2442 36.48 Pred. No. 3.86+022  
 31 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

32 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 33 111 2442 36.48 Pred. No. 3.86+022  
 34 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

35 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 36 111 2442 36.48 Pred. No. 3.86+022  
 37 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

1 PRIOR APPLICATION NUMBER: 1998-08-24  
 2 PRIOR FILING DATE: 1997-08-27  
 3 PRIOR FILING DATE: 1997-08-27  
 4 SOFTWARE: PATOUT VORSTION 4.0  
 5 SEQ ID NO: 0  
 6 LENGTH: 2442  
 7 TYPE: PRT  
 8 ORGANISM: human  
 9 US: 10 109 886 10

11 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 12 111 2442 36.48 Pred. No. 3.86+022  
 13 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

14 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 15 111 2442 36.48 Pred. No. 3.86+022  
 16 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

17 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 18 111 2442 36.48 Pred. No. 3.86+022  
 19 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

20 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 21 111 2442 36.48 Pred. No. 3.86+022  
 22 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

23 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 24 111 2442 36.48 Pred. No. 3.86+022  
 25 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

26 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 27 111 2442 36.48 Pred. No. 3.86+022  
 28 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

29 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 30 111 2442 36.48 Pred. No. 3.86+022  
 31 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1

32 111 2442 30.18 Score 47.92 DB 12 Length 2442  
 33 111 2442 36.48 Pred. No. 3.86+022  
 34 Matches 125 Conservative 5 Mismatches 9 Indels 7 Gaps 1





















EXHIBIT A: A diagrammatic representation of the three-step process of the "three-step" model of psychoplasticity (by similarity).

THE SWISS PATENT OFFICE is copyrightable if produced through a collaboration between a Swiss Post or a Bioinformatics and the SMI contribution to the Bioinformatics Institute. There are no restrictions on what is used for the Institute's institutions as long as its collection is in modified and this statement is not removed. Used by and for commercial purposes. The Swiss Patent Office is not responsible for the use of the collection of the Swiss Patent Office. If you are interested in the collection of the Swiss Patent Office, please contact the Swiss Patent Office at [info@swisspatent.ch](mailto:info@swisspatent.ch).

[illegible]

	20.5%	Score 45	DB 1	length 206
Test local similarity	42.98		Prod. NO. 23	
Method 11	generative	4	Mismatch	9
			caps	0

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

MEASURING HUMAN  
CAPABILITY

	NAME OF ORGAN	STANDARD	PRICE	475 AD.
At	Food at			
11	IRON [red] [red] 24 [red]			
11	of IRON food [red] 29's last sequence update)			
11	food [red] 29's last allocation update)			
16	Mastin protein food (Protease inhibitor 5).			
18	protein food 1.02			

[illegible][illegible][illegible]

PERTAINING TO THE SUBSTRATES IT BLOCKS THE GROWTH, INVASION, AND METASTASIS OF CELLULAR CARCINOMAS AS WELL AS EXHIBITS ANTICARCINOGENIC EFFECTS IN RELAXED CONFORMATIONAL TRANSITION CHARACTERISTICS OF ACTIVE SERPINS. IT EXHIBITS NO SIGNIFICANT INHIBITORY ACTIVITY AGAINST THE ENZYME ACTIVITY OF SERPINS. EXTRACTED FROM THE SERPINS FAMILY, IT BELONGS TO THE SERPIN FAMILY, OR SERPIN SUPERFAMILY.

The European Information Institute. There are no restrictions on its

used by non-profit institutions for as little as \$100,000 modified and this statement is not repeated by and for certain of our clients to indicate a decrease of 50% in the amount of money sold in email to Internet (sh-shi.ch).

```

DE FMID: 004113; AAID:007.1; -
DE HNSP: 005619; IHL:
DE CHNW: HNC:0443; SERP:MS.
DE MEM: 154790; -
DE INTERPR: IPR000240; MASP:n
DE IPR:000000; IPR000215; Scp:n
DE FLAG: P000079; Scp:n; I.

```

Accession	Protein	Score	Similarity
IR	SMART: SM00034; SERPIN: 1.		
IR	PROSITE: PS01284; SERPIN: 1.		
KW	Serpin; Glycoprotein; Signal.		
FP	SIGNAL	1	2
ET	CHAIN	2	375
ET	ATT_SITE	240	341
ET	CASEIN	53	59
ET	MASTEN		
ET	REACTIVE SITE (IN SIMILARITY).		
ET	REACTIVE SITE (IN FUNCTIONAL).		

F:		166	N- $\beta$ -NHRD-GMA MA	(POLINITIAL)
F:	CARBONYL	166	N- $\beta$ -NHRD-GMA MA	(POLINITIAL)
F:	CARBONYL	361	N- $\beta$ -NHRD-GMA MA	(POLINITIAL)
S:	SEQUENCE	378 MM	421.9% MA	1224 (99.9%) <sup>a</sup> 100% <sup>b</sup>

Year	March	28.5%	Spent	4.1%	188.1%	March	27.2%	
Best	Local	47.4%	Prod.	1.1%	188.1% <td>Local</td> <td>47.4%</td>	Local	47.4%	
March	28.5% <td>Spent</td> <td>4.1% <td>188.1% <td>March</td> <td>27.2% <td>Spent</td> <td>4.1% </td></td></td></td>	Spent	4.1% <td>188.1% <td>March</td> <td>27.2% <td>Spent</td> <td>4.1% </td></td></td>	188.1% <td>March</td> <td>27.2% <td>Spent</td> <td>4.1% </td></td>	March	27.2% <td>Spent</td> <td>4.1% </td>	Spent	4.1%

187. INTERNATIONAL YEAR 2005

RESULT 13	
PAC1_HUMAN	
120 PAC1_HUMAN	STANDARD:
AC Q9BYT1; Q9PZG8;	PROT 444 AA.

14F Protein kinase C and casein kinase substrate in myotubes protein 1.  
 15F Protein Cdk KAPPA.379.  
 16F  
 17F  
 18F  
 19F  
 20F  
 21F  
 22F  
 23F  
 24F  
 25F  
 26F  
 27F  
 28F  
 29F  
 30F  
 31F  
 32F  
 33F  
 34F  
 35F  
 36F  
 37F  
 38F  
 39F  
 40F  
 41F  
 42F  
 43F  
 44F  
 45F  
 46F  
 47F  
 48F  
 49F  
 50F  
 51F  
 52F  
 53F  
 54F  
 55F  
 56F  
 57F  
 58F  
 59F  
 60F  
 61F  
 62F  
 63F  
 64F  
 65F  
 66F  
 67F  
 68F  
 69F  
 70F  
 71F  
 72F  
 73F  
 74F  
 75F  
 76F  
 77F  
 78F  
 79F  
 80F  
 81F  
 82F  
 83F  
 84F  
 85F  
 86F  
 87F  
 88F  
 89F  
 90F  
 91F  
 92F  
 93F  
 94F  
 95F  
 96F  
 97F  
 98F  
 99F  
 100F

602 E. KAYOCCA, Montgomery, Georgia; *Trifolium*; Vernalis; Petaloid Stems;  
603 603 Mammalia; Furbertia; Prunellae; Catarrhini; Homiidae; Homo;  
604 NCBI; 1990; 9406;  
605 1;  
606 1;  
607 SEQUENCED FROM N.A.  
608 REF MEDLINE=21100457; PubMed=1174664  
609 EX Smoly N. J.; Furbert R.; Andrew N.; and Felli G.; *Trifolium* M.;  
610 1992; 1; 1;  
611 1992; 1; 1;  
612 1992; 1; 1;  
613 1992; 1; 1;  
614 1992; 1; 1;  
615 1992; 1; 1;  
616 1992; 1; 1;  
617 1992; 1; 1;  
618 1992; 1; 1;  
619 1992; 1; 1;  
620 1992; 1; 1;  
621 1992; 1; 1;  
622 1992; 1; 1;  
623 1992; 1; 1;  
624 1992; 1; 1;  
625 1992; 1; 1;  
626 1992; 1; 1;  
627 1992; 1; 1;  
628 1992; 1; 1;  
629 1992; 1; 1;  
630 1992; 1; 1;  
631 1992; 1; 1;  
632 1992; 1; 1;  
633 1992; 1; 1;  
634 1992; 1; 1;  
635 1992; 1; 1;  
636 1992; 1; 1;  
637 1992; 1; 1;  
638 1992; 1; 1;  
639 1992; 1; 1;  
640 1992; 1; 1;  
641 1992; 1; 1;  
642 1992; 1; 1;  
643 1992; 1; 1;  
644 1992; 1; 1;  
645 1992; 1; 1;  
646 1992; 1; 1;  
647 1992; 1; 1;  
648 1992; 1; 1;  
649 1992; 1; 1;  
650 1992; 1; 1;  
651 1992; 1; 1;  
652 1992; 1; 1;  
653 1992; 1; 1;  
654 1992; 1; 1;  
655 1992; 1; 1;  
656 1992; 1; 1;  
657 1992; 1; 1;  
658 1992; 1; 1;  
659 1992; 1; 1;  
660 1992; 1; 1;  
661 1992; 1; 1;  
662 1992; 1; 1;  
663 1992; 1; 1;  
664 1992; 1; 1;  
665 1992; 1; 1;  
666 1992; 1; 1;  
667 1992; 1; 1;  
668 1992; 1; 1;  
669 1992; 1; 1;  
670 1992; 1; 1;  
671 1992; 1; 1;  
672 1992; 1; 1;  
673 1992; 1; 1;  
674 1992; 1; 1;  
675 1992; 1; 1;  
676 1992; 1; 1;  
677 1992; 1; 1;  
678 1992; 1; 1;  
679 1992; 1; 1;  
680 1992; 1; 1;  
681 1992; 1; 1;  
682 1992; 1; 1;  
683 1992; 1; 1;  
684 1992; 1; 1;  
685 1992; 1; 1;  
686 1992; 1; 1;  
687 1992; 1; 1;  
688 1992; 1; 1;  
689 1992; 1; 1;  
690 1992; 1; 1;  
691 1992; 1; 1;  
692 1992; 1; 1;  
693 1992; 1; 1;  
694 1992; 1; 1;  
695 1992; 1; 1;  
696 1992; 1; 1;  
697 1992; 1; 1;  
698 1992; 1; 1;  
699 1992; 1; 1;  
700 1992; 1; 1;  
701 1992; 1; 1;  
702 1992; 1; 1;  
703 1992; 1; 1;  
704 1992; 1; 1;  
705 1992; 1; 1;  
706 1992; 1; 1;  
707 1992; 1; 1;  
708 1992; 1; 1;  
709 1992; 1; 1;  
710 1992; 1; 1;  
711 1992; 1; 1;  
712 1992; 1; 1;  
713 1992; 1; 1;  
714 1992; 1; 1;  
715 1992; 1; 1;  
716 1992; 1; 1;  
717 1992; 1; 1;  
718 1992; 1; 1;  
719 1992; 1; 1;  
720 1992; 1; 1;  
721 1992; 1; 1;  
722 1992; 1; 1;  
723 1992; 1; 1;  
724 1992; 1; 1;  
725 1992; 1; 1;  
726 1992; 1; 1;  
727 1992; 1; 1;  
728 1992; 1; 1;  
729 1992; 1; 1;  
730 1992; 1; 1;  
731 1992; 1; 1;  
732 1992; 1; 1;  
733 1992; 1; 1;  
734 1992; 1; 1;  
735 1992; 1; 1;  
736 1992; 1; 1;  
737 1992; 1; 1;  
738 1992; 1; 1;  
739 1992; 1; 1;  
740 1992; 1; 1;  
741 1992; 1; 1;  
742 1992; 1; 1;  
743 1992; 1; 1;  
744 1992; 1; 1;  
745 1992; 1; 1;  
746 1992; 1; 1;  
747 1992; 1; 1;  
748 1992; 1; 1;  
749 1992; 1; 1;  
750 1992; 1; 1;  
751 1992; 1; 1;  
752 1992; 1; 1;  
753 1992; 1; 1;  
754 1992; 1; 1;  
755 1992; 1; 1;  
756 1992; 1; 1;  
757 1992; 1; 1;  
758 1992; 1; 1;  
759 1992; 1; 1;  
760 1992; 1; 1;  
761 1992; 1; 1;  
762 1992; 1; 1;  
763 1992; 1; 1;  
764 1992; 1; 1;  
765 1992; 1; 1;  
766 1992; 1; 1;  
767 1992; 1; 1;  
768 1992; 1; 1;  
769 1992; 1; 1;  
770 1992; 1; 1;  
771 1992; 1; 1;  
772 1992; 1; 1;  
773 1992; 1; 1;  
774 1992; 1; 1;  
775 1992; 1; 1;  
776 1992; 1; 1;  
777 1992; 1; 1;  
778 1992; 1; 1;  
779 1992; 1; 1;  
780 1992; 1; 1;  
781 1992; 1; 1;  
782 1992; 1; 1;  
783 1992; 1; 1;  
784 1992; 1; 1;  
785 1992; 1; 1;  
786 1992; 1; 1;  
787 1992; 1; 1;  
788 1992; 1; 1;  
789 1992; 1; 1;  
790 1992; 1; 1;  
791 1992; 1; 1;  
792 1992; 1; 1;  
793 1992; 1; 1;  
794 1992; 1; 1;  
795 1992; 1; 1;  
796 1992; 1; 1;  
797 1992; 1; 1;  
798 1992; 1; 1;  
799 1992; 1; 1;  
800 1992; 1; 1;  
801 1992; 1; 1;  
802 1992; 1; 1;  
803 1992; 1; 1;  
804 1992; 1; 1;  
805 1992; 1; 1;  
806 1992; 1; 1;  
807 1992; 1; 1;  
808 1992; 1; 1;  
809 1992; 1; 1;  
810 1992; 1; 1;  
811 1992; 1; 1;  
812 1992; 1; 1;  
813 1992; 1; 1;  
814 1992; 1; 1;  
815 1992; 1; 1;  
816 1992; 1; 1;  
817 1992; 1; 1;  
818 1992; 1; 1;  
819 1992; 1; 1;  
820 1992; 1; 1;  
821 1992; 1; 1;  
822 1992; 1; 1;  
823 1992; 1; 1;  
824 1992; 1; 1;  
825 1992; 1; 1;  
826 1992; 1; 1;  
827 1992; 1; 1;  
828 1992; 1; 1;  
829 1992; 1; 1;  
830 1992; 1; 1;  
831 1992; 1; 1;  
832 1992; 1; 1;  
833 1992; 1; 1;  
834 1992; 1; 1;  
835 1992; 1; 1;  
836 1992; 1; 1;  
837 1992; 1; 1;  
838 1992; 1; 1;  
839 1992; 1; 1;  
84

R1 parashin synapsin-1/PAOP-2 group 1 family 19-2  
 R2 Gene 29,2199-205(2001).  
 R3 121  
 R4  
 R5 SEQUENCE FROM N.A.  
 R6  
 R7  
 R8  
 R9  
 R10  
 R11  
 R12  
 R13  
 R14  
 R15  
 R16  
 R17  
 R18  
 R19  
 R20  
 R21  
 R22  
 R23  
 R24  
 R25  
 R26  
 R27  
 R28  
 R29  
 R30  
 R31  
 R32  
 R33  
 R34  
 R35  
 R36  
 R37  
 R38  
 R39  
 R40  
 R41  
 R42  
 R43  
 R44  
 R45  
 R46  
 R47  
 R48  
 R49  
 R50  
 R51  
 R52  
 R53  
 R54  
 R55  
 R56  
 R57  
 R58  
 R59  
 R60  
 R61  
 R62  
 R63  
 R64  
 R65  
 R66  
 R67  
 R68  
 R69  
 R70  
 R71  
 R72  
 R73  
 R74  
 R75  
 R76  
 R77  
 R78  
 R79  
 R80  
 R81  
 R82  
 R83  
 R84  
 R85  
 R86  
 R87  
 R88  
 R89  
 R90  
 R91  
 R92  
 R93  
 R94  
 R95  
 R96  
 R97  
 R98  
 R99  
 R100  
 R101  
 R102  
 R103  
 R104  
 R105  
 R106  
 R107  
 R108  
 R109  
 R110  
 R111  
 R112  
 R113  
 R114  
 R115  
 R116  
 R117  
 R118  
 R119  
 R120  
 R121  
 R122  
 R123  
 R124  
 R125  
 R126  
 R127  
 R128  
 R129  
 R130  
 R131  
 R132  
 R133  
 R134  
 R135  
 R136  
 R137  
 R138  
 R139  
 R140  
 R141  
 R142  
 R143  
 R144  
 R145  
 R146  
 R147  
 R148  
 R149  
 R150  
 R151  
 R152  
 R153  
 R154  
 R155  
 R156  
 R157  
 R158  
 R159  
 R160  
 R161  
 R162  
 R163  
 R164  
 R165  
 R166  
 R167  
 R168  
 R169  
 R170  
 R171  
 R172  
 R173  
 R174  
 R175  
 R176  
 R177  
 R178  
 R179  
 R180  
 R181  
 R182  
 R183  
 R184  
 R185  
 R186  
 R187  
 R188  
 R189  
 R190  
 R191  
 R192  
 R193  
 R194  
 R195  
 R196  
 R197  
 R198  
 R199  
 R200  
 R201  
 R202  
 R203  
 R204  
 R205  
 R206  
 R207  
 R208  
 R209  
 R210  
 R211  
 R212  
 R213  
 R214  
 R215  
 R216  
 R217  
 R218  
 R219  
 R220  
 R221  
 R222  
 R223  
 R224  
 R225  
 R226  
 R227  
 R228  
 R229  
 R230  
 R231  
 R232  
 R233  
 R234  
 R235  
 R236  
 R237  
 R238  
 R239  
 R240  
 R241  
 R242  
 R243  
 R244  
 R245  
 R246  
 R247  
 R248  
 R249  
 R250  
 R251  
 R252  
 R253  
 R254  
 R255  
 R256  
 R257  
 R258  
 R259  
 R260  
 R261  
 R262  
 R263  
 R264  
 R265  
 R266  
 R267  
 R268  
 R269  
 R270  
 R271  
 R272  
 R273  
 R274  
 R275  
 R276  
 R277  
 R278  
 R279  
 R280  
 R281  
 R282  
 R283  
 R284  
 R285  
 R286  
 R287  
 R288  
 R289  
 R290  
 R291  
 R292  
 R293  
 R294  
 R295  
 R296  
 R297  
 R298  
 R299  
 R300  
 R301  
 R302  
 R303  
 R304  
 R305  
 R306  
 R307  
 R308  
 R309  
 R310  
 R311  
 R312  
 R313  
 R314  
 R315  
 R316  
 R317  
 R318  
 R319  
 R320  
 R321  
 R322  
 R323  
 R324  
 R325  
 R326  
 R327  
 R328  
 R329  
 R330  
 R331  
 R332  
 R333  
 R334  
 R335  
 R336  
 R337  
 R338  
 R339  
 R340  
 R341  
 R342  
 R343  
 R344  
 R345  
 R346  
 R347  
 R348  
 R349  
 R350  
 R351  
 R352  
 R353  
 R354  
 R355  
 R356  
 R357  
 R358  
 R359  
 R360  
 R361  
 R362  
 R363  
 R364  
 R365  
 R366  
 R367  
 R368  
 R369  
 R370  
 R371  
 R372  
 R373  
 R374  
 R375  
 R376  
 R377  
 R378  
 R379  
 R380  
 R381  
 R382  
 R383  
 R384  
 R385  
 R386  
 R387  
 R388  
 R389  
 R390  
 R391  
 R392  
 R393  
 R394  
 R395  
 R396  
 R397  
 R398  
 R399  
 R400  
 R401  
 R402  
 R403  
 R404  
 R405  
 R406  
 R407  
 R408  
 R409  
 R410  
 R411  
 R412  
 R413  
 R414  
 R415  
 R416  
 R417  
 R418  
 R419  
 R420  
 R421  
 R422  
 R423  
 R424  
 R425  
 R426  
 R427  
 R428  
 R429  
 R430  
 R431  
 R432  
 R433  
 R434  
 R435  
 R436  
 R437  
 R438  
 R439  
 R440  
 R441  
 R442  
 R443  
 R444  
 R445  
 R446  
 R447  
 R448  
 R449  
 R450  
 R451  
 R452  
 R453  
 R454  
 R455  
 R456  
 R457  
 R458  
 R459  
 R460  
 R461  
 R462  
 R463  
 R464  
 R465  
 R466  
 R467  
 R468  
 R469  
 R470  
 R471  
 R472  
 R473  
 R474  
 R475  
 R476  
 R477  
 R478  
 R479  
 R480  
 R481  
 R482  
 R483  
 R484  
 R485  
 R486  
 R487  
 R488  
 R489  
 R490  
 R491  
 R492  
 R493  
 R494  
 R495  
 R496  
 R497  
 R498  
 R499  
 R500  
 R501  
 R502  
 R503  
 R504  
 R505  
 R506  
 R507  
 R508  
 R509  
 R510  
 R511  
 R512  
 R513  
 R514  
 R515  
 R516  
 R517  
 R518  
 R519

NI for large proteins in vitro." *J. Biol. Chem.* 265:7365-7368 (1990).

NI DNA Pos. 7:65-73(2000).

NI 131

NI SEQUENCE FROM N.A.

NI PROSOD: Amygdala;

NI Olfenkellet P.; Ventralot R.; Moore H. W.; Wotz H.; Wiedmann S.; Schottkeld J. (1992) Is the hippocampus a product of the telencephalon?

NI 41

NI PRODUCTION.

**PX** PubMed 10820447  
**RA** Kallenberg JG, Rietter Bos WJ, de Looze M, Flomijn-Meysman RM, van Halbeek H  
**KE** "At least three PASTIN isoforms bind to embryonic proteins and inhibit"



© 2004 Blackwell Publishing Ltd *Journal of Internal Medicine* 255: 399–406

•  
•  
•





```

1  nucleotide to bacterial species subdivision: Helicobacter group
2  Helicobacter
3  Nucleotide
4  Nucleotide
5  Nucleotide
6  Nucleotide
7  Nucleotide
8  Nucleotide
9  Nucleotide
10 Nucleotide
11 Nucleotide
12 Nucleotide
13 Nucleotide
14 Nucleotide
15 Nucleotide
16 Nucleotide
17 Nucleotide
18 Nucleotide
19 Nucleotide
20 Nucleotide
21 Nucleotide
22 Nucleotide
23 Nucleotide
24 Nucleotide
25 Nucleotide
26 Nucleotide
27 Nucleotide
28 Nucleotide
29 Nucleotide
30 Nucleotide
31 Nucleotide
32 Nucleotide
33 Nucleotide
34 Nucleotide
35 Nucleotide
36 Nucleotide
37 Nucleotide
38 Nucleotide
39 Nucleotide
40 Nucleotide
41 Nucleotide
42 Nucleotide
43 Nucleotide
44 Nucleotide
45 Nucleotide
46 Nucleotide
47 Nucleotide
48 Nucleotide
49 Nucleotide
50 Nucleotide
51 Nucleotide
52 Nucleotide
53 Nucleotide
54 Nucleotide
55 Nucleotide
56 Nucleotide
57 Nucleotide
58 Nucleotide
59 Nucleotide
60 Nucleotide
61 Nucleotide
62 Nucleotide
63 Nucleotide
64 Nucleotide
65 Nucleotide
66 Nucleotide
67 Nucleotide
68 Nucleotide
69 Nucleotide
70 Nucleotide
71 Nucleotide
72 Nucleotide
73 Nucleotide
74 Nucleotide
75 Nucleotide
76 Nucleotide
77 Nucleotide
78 Nucleotide
79 Nucleotide
80 Nucleotide
81 Nucleotide
82 Nucleotide
83 Nucleotide
84 Nucleotide
85 Nucleotide
86 Nucleotide
87 Nucleotide
88 Nucleotide
89 Nucleotide
90 Nucleotide
91 Nucleotide
92 Nucleotide
93 Nucleotide
94 Nucleotide
95 Nucleotide
96 Nucleotide
97 Nucleotide
98 Nucleotide
99 Nucleotide
100 Nucleotide

```

[illegible]







